

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:11 ; Search time 33 Seconds

(without alignments)
429.846 Million cell updates/sec

Title: US-09-835-922-2

Perfect score: 1778
Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SODNRKEDGDPNEETPM 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	342	P2YC_HUMAN	Q9H244 homo sapien
2	1748	98.3	342	P2YC_MACEA	Q95K63 macaca fasc
3	1555.5	87.5	347	P2YC_MOUSE	Q9EPY9 mus musculu
4	1528.5	86.0	343	P2YC_RAT	Q9EPY4 rattus norv
5	772	43.4	338	P2YX_HUMAN	Q15391 homo sapien
6	741.5	41.7	338	P2YX_MOUSE	Q9ES96 mus musculu
7	694	39.0	305	P2YX_RAT	Q35881 rattus norv
8	488	27.4	319	H963_HUMAN	Q14626 homo sapien
9	411.5	23.1	375	GP34_MOUSE	Q9R1K6 mus musculu
10	409.5	23.0	361	GP34_HUMAN	Q9UP65 homo sapien
11	394	22.2	342	PAFR_HUMAN	P25105 homo sapien
12	392.5	22.1	342	PAFR_CAVPO	P21556 cavia porce
13	379.5	21.3	361	EBI2_HUMAN	P32249 homo sapien
14	367	20.6	345	CLT2_PIG	Q95N03 sus scrofa
15	365	20.6	341	PAFR_MOUSE	Q62035 mus musculu
16	362	20.4	341	PAFR_RAT	P46002 rattus norv
17	357.5	20.1	308	P2Y5_CHICK	P32250 gallus gall
18	347.5	19.5	346	CLT2_HUMAN	Q9AS75 homo sapien
19	347.5	19.5	537	P2Y8_XENLA	P79928 xenopus lae
20	344	19.3	309	CLT2_MOUSE	Q92081 mus musculu
21	339.5	19.1	309	CLT2_RAT	Q92469 rattus norv
22	339	19.1	359	AG2R_BOVIN	P25104 bos taurus
23	338	19.0	344	P2Y5_HUMAN	P33657 homo sapien
24	334	18.8	359	AG2R_SHEEP	Q77590 ovis aries
25	334	18.8	367	GP17_HUMAN	Q13304 homo sapien
26	329	18.5	359	AG2S_HUMAN	Q13725 homo sapien
27	328	18.4	340	CLT1_PIG	Q95N02 sus scrofa
28	327	18.4	359	AG2R_PIG	P30555 sus scrofa
29	326	18.3	359	AG2R_CANFA	P33240 canis famli
30	325.5	18.3	359	PAR2_MOUSE	P53066 mus musculu
31	325	18.3	359	AG2R_RABIT	P43976 corycolagus
32	321	18.1	359	AG2R_HUMAN	P30556 homo sapien
33	320	18.0	359	AG2R_CAVPO	Q9W26 cavia porce

34	320	18.0	370	1	P2Y9_HUMAN	Q96677 homo sapien
35	319.5	18.0	365	1	GP68_HUMAN	Q15743 homo sapien
36	319	17.9	359	1	AG2R_RAT	P25095 rattus norv
37	319	17.9	359	1	AG2S_RAT	P29089 rattus norv
38	318	17.9	359	1	AG2R_MOUSE	P29754 mus musculu
39	318	17.9	361	1	P2Y4_MOUSE	Q91167 mus musculu
40	316.5	17.8	358	1	OPRM_RAT	P33535 rattus norv
41	316	17.8	359	1	AG2S_MOUSE	P29755 mus musculu
42	316	17.8	377	1	APJ_RAT	Q91H93 rattus norv
43	316	17.8	397	1	PAR2_RAT	Q63645 rattus norv
44	313.5	17.6	380	1	APJ_HUMAN	P35414 homo sapien
45	313.5	17.6	401	1	OPRM_PIG	Q95247 sus scrofa

ALIGNMENTS

RESULT 1
ID P2YC_HUMAN STANDARD: PRT; 342 AA.
AC Q9H244;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinocceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y(ADP))
DE (ADP-glucose receptor) (ADPG-R) (P2Y(AC)) (P2Y(CYC)) (P2Y(AC))
DE (SP1999).
GN P2RY12 OR HORR3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21037966; PubMed-11196645;
RA Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan D.J.,
RA Conley P.B.;
RT "Identification of the platelet ADP receptor targeted by
RT antithrombotic drugs";
RL Nature 409:202-207(2001).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RX MEDLINE-21269433; PubMed-11104774;
RA Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,
RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,
RA Mensa F.J. Jr.;
RT "ADP is the cognate ligand for the orphan G protein-coupled receptor
RT SP1999";
RL J. Biol. Chem. 276:8608-8615(2001).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-21394281; PubMed-11502873;
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.-I.,
RA Ohishi T., Soga T., Matsushima H., Furutachi K.;
RT "Molecular cloning of the platelet P2Y(AC) ADP receptor:
RT pharmacological comparison with another ADP receptor, the P2Y1
RT receptor";
RL Mol. Pharmacol. 60:432-439(2001).
[4]
RP SEQUENCE FROM N.A.
RA Reinscheid R.K., Notthacker H.-P., Wang Z., Zeng J., Ehler F.J.,
RA Clivelli O.;
RT "ADP-glucose activates a G-protein coupled receptor and inhibits
RT smooth muscle contractions";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takase H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RP [6]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Prostate;
 RA Strausberg R;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
 CC inhibit the adenylyl cyclase second messenger system. Not
 CC activated by UDP and UTP. Involved in platelets aggregation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the platelets, lower
 CC levels in the brain. Lowest levels in the lung, appendix,
 CC pituitary and adrenal gland. Expressed in the spinal cord and in
 CC the fetal brain.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: AF314448; AAG48944.1; -
 CC EMBL: AF321815; AAK00948.1; -
 CC EMBL: AB052684; BAB60824.1; -
 CC EMBL: AF310685; AAL32292.1; -
 CC EMBL: AB083596; BAB89309.1; -
 CC EMBL: BC017898; AAH17898.1; -
 CC MIM: 600515; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCR_RHODOPSIN.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 CC PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; glycoprotein.
 CC DOMAIN 1
 CC TRANSMEM 26 46
 CC FT TRANSMEM 47 58
 CC FT TRANSMEM 59 79
 CC FT TRANSMEM 80 99
 CC FT TRANSMEM 100 120
 CC FT TRANSMEM 121 142
 CC FT TRANSMEM 143 163
 CC FT TRANSMEM 164 191
 CC FT TRANSMEM 192 212
 CC FT TRANSMEM 213 233
 CC FT TRANSMEM 234 254
 CC FT TRANSMEM 255 281
 CC FT TRANSMEM 282 302
 CC FT TRANSMEM 303 342
 CC FT DISULFID 97 175
 CC FT CARBOHYD 6 6
 CC FT CARBOHYD 13 13
 CC SEQUENCE 342 AA; 39438 MW; 8553D2746C89176D CRC64;
 CC
 CC Query Match 100.0%; Score 1778; DB 1; Length 342;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-112;
 CC Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 EFGVWHEIYVNYICQYEWINEFLIVCYTLITKELYSRYTRGVGKVRKKVKKYFI 240
 DB 181 EFGVWHEIYVNYICQYEWINEFLIVCYTLITKELYSRYTRGVGKVRKKVKKYFI 240
 QY 241 IIAVFVFCVPPHFAPIPTLSQTRDVFDCIENLIFYKESSTLWLSINACLDPIFYF 300
 DB 241 IIAVFVFCVPPHFAPIPTLSQTRDVFDCIENLIFYKESSTLWLSINACLDPIFYF 300
 QY 301 LCKSPFNSLISMLKCPNSATSLSDNRKKEODGSDPNEETPM 342
 DB 301 LCKSPFNSLISMLKCPNSATSLSDNRKKEODGSDPNEETPM 342
 RESULT 2
 P2YC_MACFA STANDARD; PRT; 342 AA.
 AC 095KC3; 09BGT8;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 12 (P2Y12).
 GN P2RY12.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Frontal cortex, and Medulla oblongata;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
 CC inhibit the adenylyl cyclase second messenger system (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AB056385; BAB33041.1; -
 CC EMBL: AB062981; BAB60747.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCR_RHODOPSIN.
 CC PRINTS: PR01659; P2Y12_PNCPT.
 CC PRINTS: PR01655; UDPGLUCOSE.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 CC PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; glycoprotein.
 CC DOMAIN 1
 CC TRANSMEM 26 46
 CC FT TRANSMEM 47 58
 CC FT TRANSMEM 59 79
 CC FT TRANSMEM 80 99
 CC FT TRANSMEM 100 120
 CC FT TRANSMEM 121 142
 CC FT TRANSMEM 143 163
 CC FT TRANSMEM 164 191
 CC FT TRANSMEM 192 212
 CC FT TRANSMEM 213 233
 CC FT TRANSMEM 234 254
 CC FT TRANSMEM 255 281
 CC FT TRANSMEM 282 302

XX (HUMA-) HUMAN GENOME SCI INC.
XX L1 Y, Ruben SM;
XX WPI: 1999-034722/03.
DR N-PSDB: AAV69760.
XX
XX
XX New isolated human G-protein coupled receptors - used to develop
XX products for treating e.g. asthma, Parkinson's disease, heart
XX failure, osteoporosis, hypertension, psychoses, eating disorders or
XX cancers
XX
XX Claim 1; Fig 1A-C; 65pp; English.
XX
XX This represents a EBV-induced G-protein coupled receptor (EBI-2)
XX polypeptide. The encoding DNA is deposited under the accession number
XX ATCC No: 209003. The invention provides two human G-protein coupled
XX receptor polypeptides. The polypeptides are human Epstein-Barr Virus
XX (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide
XX and a human endothelium-differentiation gene (EDG) like G-protein coupled
XX receptor, designated EDG-1-like G-protein coupled receptor. Vectors
XX comprising the EBI-2 and EDG-1-like polypeptides encoding DNA can be used
XX to transform host cells for the recombinant production of the proteins.
XX Agonists for G-protein coupled receptors can be used for the treatment of
XX asthma, Parkinson's disease, acute heart failure, hypertension, urinary
XX retention and osteoporosis. Antagonists can be used for the treatment of
XX hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
XX allergies, psychoses, depression, migraine, vomiting, stroke, eating
XX disorders, migraine headaches, cancer and benign prostatic hypertrophy.
XX The products can also be used for detection, diagnosis and drug
XX screening.
XX
XX Sequence 342 AA;
SQ
Query Match 100.0%; Score 1778; DB 20; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYLVLFVGLITNGLAMRIFFOIRSKSNFI 60
DB 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYLVLFVGLITNGLAMRIFFOIRSKSNFI 60
QY 61 IELNNTVSDMLITLTPFKILSDAKLGTGRLTFVQVSVITFYFYIISFLGLTTI 120
DB 61 IFLNNTVSDMLITLTPFKILSDAKLGTGRLTFVQVSVITFYFYIISFLGLTTI 120
QY 121 DRYOCTTREPFTSNPKNLGAKILSVIWMFMFLSLPMLITNROPDKNVKCSFLKS 180
DB 121 DRYOCTTREPFTSNPKNLGAKILSVIWMFMFLSLPMLITNROPDKNVKCSFLKS 180
QY 181 EFGLVMEIIVNYICQVIFWIMFLIIVCYTLITRELYRSYVRGKVPKRVNVKVEI 240
DB 181 EFGLVMEIIVNYICQVIFWIMFLIIVCYTLITRELYRSYVRGKVPKRVNVKVEI 240
QY 241 IIAVFCEVFEHFAHRIPTLTSTQRDVFDCAEHTLLEFVKKSTLMLSLNACLDPIYIF 300
DB 241 IIAVFCEVFEHFAHRIPTLTSTQRDVFDCAEHTLLEFVKKSTLMLSLNACLDPIYIF 300
QY 301 LCKSFRLNLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
DB 301 LCKSFRLNLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
RESULT 2
ID AAV71306 standard; Protein: 342 AA.
XX
XX AAV71306;
XX
XX 02-NOV-2000 (first entry)
XX Human orphan G protein-coupled receptor hCHN8.

XX Human: orphan G protein-coupled receptor; GPCR; hCHN8; drug screening;
XX transmembrane receptor; expressed sequence tag; EST; signal cascade.
XX
XX Homo sapiens.
XX W0200031258-A2.
XX
XX
XX 02-JUN-2000.
XX
XX
XX 13-OCT-1999; 99WO-US23687.
XX
XX 20-NOV-1998; 98US-0109213.
XX 16-FEB-1999; 99US-0120416.
XX 26-FEB-1999; 99US-0121852.
XX 12-MAR-1999; 99US-0123946.
XX 12-MAR-1999; 99US-0123949.
XX 28-MAY-1999; 99US-0136436.
XX 28-MAY-1999; 99US-0136437.
XX 28-MAY-1999; 99US-0136439.
XX 28-MAY-1999; 99US-0136567.
XX 28-MAY-1999; 99US-0137127.
XX 28-MAY-1999; 99US-0137131.
XX 29-JUN-1999; 99US-0141448.
XX 29-SEP-1999; 99US-0156555.
XX 29-SEP-1999; 99US-0156557.
XX 29-SEP-1999; 99US-0156633.
XX 29-SEP-1999; 99US-0156653.
XX 29-SEP-1999; 99US-0156653.
XX 01-OCT-1999; 99US-0157280.
XX 01-OCT-1999; 99US-0157281.
XX 01-OCT-1999; 99US-0157282.
XX 01-OCT-1999; 99US-0157293.
XX 01-OCT-1999; 99US-0157294.
XX 12-OCT-1999; 99US-0416760.
XX 12-OCT-1999; 99US-0417044.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Chen R, Dang HT, Llaw CW, Lin I;
XX WPI: 2000-400068/34.
XX N-PSDB: AAD01133.
XX
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs
XX for use in the identification of G protein-coupled receptor agonists -
XX
XX Claim 62; Page 82-83; 102pp; English.
XX
XX The present amino acid sequence is the hCHN8, an endogenous human
XX orphan G protein-coupled receptor (GPCR), expressed in left and right
XX cerebellum, kidney and lung. The hCHN8 cDNA was identified using full
XX length EST (expressed sequence tag) 764455 as a probe.
XX The orphan GPCR of the invention, like all GPCRs has seven transmembrane
XX alpha helices with an extracellular N-terminus and an intracellular
XX C-terminus. However, no endogenous ligands has yet been identified for
XX the proteins of the invention. The orphan GPCRs may be used in the
XX identification of their endogenous ligands, and to screen potential GPCR
XX agonists and antagonists for use as pharmaceutical agents. The proteins
XX may also be used in the study of GPCR-mediated signalling cascades, and
XX to elucidate their precise role in normal and diseased human conditions.
XX Nucleic acid encoding human orphan GPCRs may be used for tissue
XX localisation expression analysis to provide information about their
XX function in healthy and pathological states.
XX
XX Sequence 342 AA;
SQ
Query Match 100.0%; Score 1778; DB 21; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYLVLFVGLITNGLAMRIFFOIRSKSNFI 60
DB 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYLVLFVGLITNGLAMRIFFOIRSKSNFI 60

```

QY 61 IFLNNTVISDLMLITPEPKILSDAKLGTPGLRTFVCQVTSVIFFTWYISISFLGLITI 120
DB 61 IFLNNTVISDLMLITPEPKILSDAKLGTPGLRTFVCQVTSVIFFTWYISISFLGLITI 120
QY 121 DRYOKTTRPEKTSNPKNLGAKILSVYIWMAPFLSLPNMLTLTRQPRDKNVKCSFLKS 180
DB 121 DRYOKTTRPEKTSNPKNLGAKILSVYIWMAPFLSLPNMLTLTRQPRDKNVKCSFLKS 180
QY 181 EFGIWMHEIVNYICQVIFWIMFLIYVCYTLITKEIYRSYVTRGVGKVPKKVNVKVEI 240
DB 181 EFGIWMHEIVNYICQVIFWIMFLIYVCYTLITKEIYRSYVTRGVGKVPKKVNVKVEI 240
QY 241 IIAVFICFVFPFHPARIPYTLISQTRDVFDCYAEWTLFVYKESSTLMLSLNACLDPEFIYFF 300
DB 241 IIAVFICFVFPFHPARIPYTLISQTRDVFDCYAEWTLFVYKESSTLMLSLNACLDPEFIYFF 300
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRRKKEDGDPNEETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRRKKEDGDPNEETPM 342

RESULT 3
AAB02840
ID AAB02840 standard; Protein: 342 AA.
XX
AC AAB02840;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hCHN8 protein SEQ ID NO:34.
XX
KM Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.
XX
OS Homo sapiens.
XX
PN WO200022131-A2.
XX
PD 20-Apr-2000.
XX
PF 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
XX (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Lehmann-Brulinsma K, Chalmers DT, Chen R, Dang HT,
Gore M, Liaw CW, Lin I, Lowitz K, White C;

```

```

XX WPI: 2000-317986/27.
DR N-PSDB: AAA46034.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PS receptor, inverse or partial agonists useful as therapeutic agents
XX
XX Example 1; Page 112-113; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (Orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 21; Length 342;
Best Local Similarity 100.0%; Pred. No. 3e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNILTSAPGNTSLCTRDYKITQVLPFLIYTVLFVGLITNGIARIRFOIRSKSNFI 60
DB 1 MQAVDNILTSAPGNTSLCTRDYKITQVLPFLIYTVLFVGLITNGIARIRFOIRSKSNFI 60
QY 61 IFLNNTVISDLMLITPEPKILSDAKLGTPGLRTFVCQVTSVIFFTWYISISFLGLITI 120
DB 61 IFLNNTVISDLMLITPEPKILSDAKLGTPGLRTFVCQVTSVIFFTWYISISFLGLITI 120
QY 121 DRYOKTTRPEKTSNPKNLGAKILSVYIWMAPFLSLPNMLTLTRQPRDKNVKCSFLKS 180
DB 121 DRYOKTTRPEKTSNPKNLGAKILSVYIWMAPFLSLPNMLTLTRQPRDKNVKCSFLKS 180
QY 181 EFGIWMHEIVNYICQVIFWIMFLIYVCYTLITKEIYRSYVTRGVGKVPKKVNVKVEI 240
DB 181 EFGIWMHEIVNYICQVIFWIMFLIYVCYTLITKEIYRSYVTRGVGKVPKKVNVKVEI 240
QY 241 IIAVFICFVFPFHPARIPYTLISQTRDVFDCYAEWTLFVYKESSTLMLSLNACLDPEFIYFF 300
DB 241 IIAVFICFVFPFHPARIPYTLISQTRDVFDCYAEWTLFVYKESSTLMLSLNACLDPEFIYFF 300
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRRKKEDGDPNEETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRRKKEDGDPNEETPM 342

RESULT 4
AAY94444
ID AAY94444 standard; Protein: 342 AA.
XX
AC AAY94444;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human 15625 receptor protein.
XX
KW Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
KW glial cells; spleen; colon; liver; brain; T-cell; heart;
KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Domain 1..25
XX Modified-site /label= extracellular_domain
XX Msc-difference 6..9 /label= N-glycosylation
XX 13

```

FT	Modified-site	/note- "encoded by ACC"
FT		13..16
FT	Domain	/label- N-glycosylation
FT		26..302
FT	Modified-site	/label- Transmembrane_domain
FT		39..44
FT	Modified-site	/label- N-myristoylation
FT		121..123
FT	Modified-site	/label- GPCR signal transduction site
FT		126..128
FT	Modified-site	/label- protein_kinase_C-phosphorylation
FT		163..165
FT	Modified-site	/label- protein_kinase_C-phosphorylation
FT		173..176
FT	Domain	/label- protein_kinase-phosphorylation
FT		303..342
FT	Modified-site	/label- Intracellular_domain
FT		304..306
FT	Modified-site	/label- protein_kinase_C-phosphorylation
FT		333..338
FT	Modified-site	/label- N-myristoylation
PN		
PD	WO200028028-A1.	
PP	18-MAY-2000.	
PX		
PR	05-NOV-1999;	99WO-US25956.
PR	06-NOV-1998;	98US-0187134.
PR	25-AUG-1999;	99US-0382918.
PA	(MILL-) MILLENNIUM PHARM INC.	
PI	Glucksmann MA, Gu W, Welch NS;	
DR	WPI: 2000-376543/32.	
XX	N-PSDB; AAA27126.	
PT	Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia	-
PS	Disclosure: Page 88-89; 97pp; English.	
XX		
CC	The present sequence shows the 15625 receptor protein. It is a novel G-coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein. The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia.	
SQ	Sequence 342 AA:	
OY	Query Match	100.0%; Score 1778; DB 21; Length 342;
	Best Local Similarity	100.0%; Pred. No. 5e-187;
	Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 MOAONLISAPENTSLGRDYKITOVLEPLATYVFPGILNGLAMRIEPOIRKSNPT 60	
Oy	61 IFLKNTVISDLMLITFPFKILSDAKKLGTGPRTVCVTSVIFFTMTSISFGLITI 120	
Ddb	61 IFLKNTVISDLMLITLPFKILSDAKKLGTGCPRTVCVTSTVFETMTSISFGLITI 120	
Oy	121 DRYQTTRPEKTSNPKNLIGAKILSVIAWFELLSPNMILTNRQPRDKNYKKCSFKS 180	

Db	121	DRQKTRPEFTSPKMLGLGAKTISVYNAFMFLSLPMLITNKPQPKKANKKSPFLKS	180
Qy	181	EFGLWMEHIVNYICQVIFWFINFLIVICYTLTKELYSVTRTGVKVPKRVKVFYI	240
Db	181	EFGLWMEHIVNYICQVIFWFINFLIVICYTLTKELYSVTRTGVKVPKRVKVFYI	240
Qy	241	IIAIFVFCFVPHFARIPYTLSTQRTQVDFCTAENTLFYKKESTLWLTSLNACLDPEIFYEF	300
Db	241	IIAIFVFCFVPHFARIPYTLSTQRTQVDFCTAENTLFYKKESTLWLTSLNACLDPEIFYEF	300
Qy	301	ICKSFNSLSIMLKCPSNATSLSODNKRKREQDGDPEETPM	342
Db	301	ICKSFNSLSIMLKCPSNATSLSODNKRKREQDGDPEETPM	342
RESULT 5			
AA	AAAM79249		
ID	AAAM79249	standard; Protein; 342 AA.	
XX	AAAM79249;		
AC			
DT	06-NOV-2001	(first entry)	
XX			
DE	Human protein SEQ ID NO 1911.		
XX			
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorder; arthritis; inflammation.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157190-A2.		
PD			
XX	09-AUG-2001.		
PF			
XX	05-FEB-2001; 2001MO-USO4098.		
XX			
PR	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693325.		
PR	30-NOV-2000; 2000US-0728422.		
XX			
PA	(HYSE-) HYSEQ INC.		
PI	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;		
PI	Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
XX			
DR	WPI: 2001-476283/51.		
DR	N-PSDB: AAK52382.		
XX			
PT	Nucleic acids encoding polypeptides with cytokine-like activities,		
PT	useful in diagnosis and gene therapy -		
XX			
PS	Claim 20; Page 4310; 6221pp: English.		
XX			
CC	The invention relates to polynucleotides (AAK51456-AAK53435) and the		
CC	encoded polypeptides (AAAM78373-AAAM80302) that exhibit actively elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activin/inhibin activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		
CC	inflammation.		

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

SO Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 22; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
DB 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFLKMTVSDLLMTLTFPPKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
DB 61 IFLKMTVSDLLMTLTFPPKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
QY 121 DRYQKTTTPFKTSNPNKILGAKILSVIWAEMFLSLPMLITNQPDKNVKCSFLKS 180
DB 121 DRYQKTTTPFKTSNPNKILGAKILSVIWAEMFLSLPMLITNQPDKNVKCSFLKS 180
QY 181 EFGLVWHEIVNYICQVIMINFLIVCYTLITKELYSYVTRGVGKVRKKVAVKFI 240
DB 181 EFGLVWHEIVNYICQVIMINFLIVCYTLITKELYSYVTRGVGKVRKKVAVKFI 240
QY 241 IIAVFICFVPPHFARIPYTLISQTRDVDCTAENTLFFVKESTLWLTSLNACLDPEFIYFF 300
DB 241 IIAVFICFVPPHFARIPYTLISQTRDVDCTAENTLFFVKESTLWLTSLNACLDPEFIYFF 300
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNETPM 342

RESULT 6
AAE04386
ID AAE04386 standard; Protein: 342 AA.
AC AAE04386;
XX
XX 04-SEP-2001 (first entry)
DE Human P2-purinegic receptor subtype, p2y12.
XX
XX Human; P2-purinegic receptor; p2y12; cardiant; vasotropic; thrombolytic; cerebroprotective; gynecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; pre-eclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angiodysplasia; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein; GI; disseminated intravascular coagulation; thrombosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT 27..50 /label= Transmembrane_domain_1
FT /label= Transmembrane_domain_1
FT 58..82 /label= Transmembrane_domain_2
FT /label= Transmembrane_domain_2
FT 97..121 /label= Transmembrane_domain_3
FT /label= Transmembrane_domain_3
FT 140..163 /label= Transmembrane_domain_4
FT /label= Transmembrane_domain_4
FT 189..213 /label= Transmembrane_domain_5
FT /label= Transmembrane_domain_5
FT 234..259 /label= Transmembrane_domain_6
FT /label= Transmembrane_domain_6
FT 278..303 /label= Transmembrane_domain_7
FT /label= Transmembrane_domain_7
XX
XX W0200146454-AA.

XX 28-JUN-2001.
PD 26-DEC-2000; 2000WO-US34998.
XX
XX 23-DEC-1999; 99US-0171622.
PR
XX (CORT-) COR THERAPEUTICS INC.
PA
PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
PI Holloper G;
XX WPI: 2001-418082/44.
DR N-PSDB: AAD08695.
XX
XX Novel isolated ADP receptor, termed p2y12 receptor polypeptide, useful
PT for identifying binding partners and for diagnostic applications -
XX
XX Example 1; Fig 5A; 108bp; English.
XX
XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
CC as p2y12 receptor and its corresponding cDNA molecule. p2y12 receptor is
CC the subtype of P2-purinegic receptor. The p2y12 receptor is expressed
CC selectively in the platelets and brain, and couples to a pertussis toxin-
CC sensitive G protein (G_i). p2y12 receptor is a G protein-coupled receptor
CC that responds to ADP. The invention also relates to a method for
CC identifying an agent which is useful for modulating acute myocardial
CC infarction, unstable angina, chronic stable angina, transient ischaemic
CC attacks, strokes, peripheral vascular disease, pre-eclampsia, deep venous
CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
CC thrombocytopenic purpura or a bleeding disorder; carotid endarterectomy,
CC restenotic complications following angioplasty, carotid endarterectomy,
CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
CC stent placements or insertion of endovascular devices and prostheses.
CC p2y12 receptor is useful for identifying binding partners and for
CC diagnostic applications. p2y12 receptor provides targets for screening
CC synthetic small molecules and combinatorial or naturally occurring
CC compound libraries to regulate platelet aggregation, vascular injury, or
CC disease as well as schizophrenia, eating disorders, depression, migraine
CC and other brain disorders. The present sequence is human P2-purinegic
CC receptor subtype, referred as p2y12.
XX
XX
XX Sequence 342 AA:
SQ
Query Match 100.0%; Score 1778; DB 22; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
DB 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFLKMTVSDLLMTLTFPPKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
DB 61 IFLKMTVSDLLMTLTFPPKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
QY 121 DRYQKTTTPFKTSNPNKILGAKILSVIWAEMFLSLPMLITNQPDKNVKCSFLKS 180
DB 121 DRYQKTTTPFKTSNPNKILGAKILSVIWAEMFLSLPMLITNQPDKNVKCSFLKS 180
QY 181 EFGLVWHEIVNYICQVIMINFLIVCYTLITKELYSYVTRGVGKVRKKVAVKFI 240
DB 181 EFGLVWHEIVNYICQVIMINFLIVCYTLITKELYSYVTRGVGKVRKKVAVKFI 240
QY 241 IIAVFICFVPPHFARIPYTLISQTRDVDCTAENTLFFVKESTLWLTSLNACLDPEFIYFF 300
DB 241 IIAVFICFVPPHFARIPYTLISQTRDVDCTAENTLFFVKESTLWLTSLNACLDPEFIYFF 300
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNETPM 342

RESULT 7

AB877868
ID ABB77868 standard; Protein; 342 AA.

XX AC ABB77868;

DT 27-SEP-2002 (first entry)

XX Amino acid sequence of human ADP receptor P2YAC protein.

XX Human; ADP receptor; P2YAC; antiplatelet agent; thrombotic disease;
KM ischaemic disease.

XX Homo sapiens.

XX WO200236631-A1.

XX 10-MAY-2002.

XX 31-OCT-2001; 2001WO-JP09534.

XX 01-NOV-2000; 2000JP-0334721.

XX 11-JAN-2001; 2001JP-0003577.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Takasaki J, Matsumoto M, Kamohara M, Saito T, Ohishi T, Soga T;

XX WPI: 2002-519236/55.

XX N-PSDB; ABL59205.

XX Method for screening anti-platelet agents with human ADP receptor P2YAC
PT protein, its functional equivalent, or its homologous protein, as tool,
PT for treating e.g. thrombotic or ischaemic diseases

XX Claim 1; Page 48-49; 56pp; Japanese.

XX The present sequence represents a human ADP receptor P2YAC protein. It is
CC used as a screening tool for screening for antiplatelet agents. The
CC method is used for screening for antiplatelet agents, which can then
CC be used for treating e.g. thrombotic or ischaemic diseases.

XX Sequence 342 AA;

XX Query Match 100.0%; Score 1778; DB 23; Length 342;

XX Best Local Similarity 100.0%; Pred. No. 5e-187;

XX Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MOAVDNLTSAAGNTSLCRODKITOVLEPLTYLFFVGLITNGIAMIFPOIRSKSNEI 60

XX 1 MOAVDNLTSAAGNTSLCRODKITOVLEPLTYLFFVGLITNGIAMIFPOIRSKSNEI 60

XX 61 IFLKNTYISDLMLTEPEFKILSDAKLGTPLRTEVCVSVIFETWYISISFLGLITI 120

XX 61 IFLKNTYISDLMLTEPEFKILSDAKLGTPLRTEVCVSVIFETWYISISFLGLITI 120

XX 121 DRYKTRPFTSNPKNLGAKIISVYIMAFMFLISLPMILNRPDKVKKCSPLKS 180

XX 121 DRYKTRPFTSNPKNLGAKIISVYIMAFMFLISLPMILNRPDKVKKCSPLKS 180

XX 121 DRYKTRPFTSNPKNLGAKIISVYIMAFMFLISLPMILNRPDKVKKCSPLKS 180

XX 181 EFGLVMEHIVYICGVFMIFELIVICYTLITKEIYRSYRTGCVGVPRKKVNVKEI 240

XX 181 EFGLVMEHIVYICGVFMIFELIVICYTLITKEIYRSYRTGCVGVPRKKVNVKEI 240

XX 181 EFGLVMEHIVYICGVFMIFELIVICYTLITKEIYRSYRTGCVGVPRKKVNVKEI 240

XX 241 IIAVEFICFVPHFARIPYTLISQTRDVFDCYAEMLFYVKESTLMLTSLNACLDPEFIYF 300

XX 241 IIAVEFICFVPHFARIPYTLISQTRDVFDCYAEMLFYVKESTLMLTSLNACLDPEFIYF 300

XX 301 LCKSFRNSLISMLKCPNSATSLSDNRRKKEDGDDPNEETPM 342

XX 301 LCKSFRNSLISMLKCPNSATSLSDNRRKKEDGDDPNEETPM 342

XX 301 LCKSFRNSLISMLKCPNSATSLSDNRRKKEDGDDPNEETPM 342

RESULT 8

AA080164
ID AA080164 standard; Protein; 342 AA.

XX AC AA080164;

DT 15-JUL-2002 (first entry)

XX Human ADP-glucose receptor.

XX Human; ADP-glucose; receptor; G protein-coupled receptor;
KM agonist; antagonist; cardiovascular function disorder; vasorelaxation;
KM ischaemia; angina pectoris; gastrointestinal disorder; diarrhoea;
KM immune disorder; immunodeficiency disorder; autoimmune disorder;
KM rheumatoid arthritis; bacterial infection; viral infection;
KM fungal infection; protozoal infection; respiratory disorder; asthma;
KM kidney disorder; glomerulonephritis; hepatobiliary disorder; cirrhosis;
KM endocrine disorder; adrenal dysfunction; musculoskeletal disorder;
KM osteoporosis; nervous system disorder; Alzheimer's disease;
KM psychotic disorder; depression; cancer; pain; glycogen storage disease;
KM disorder of body weight; AIDS; acquired immunodeficiency syndrome;
KM chromosome 3; Usher's syndrome, type 3.

XX Homo sapiens.

XX WO200224942-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US29523.

XX 20-SEP-2000; 2000US-234023P.

XX 09-FEB-2001; 2001US-0780576.

XX (REGC) UNIV CALIFORNIA.

XX Clivelli O, Notackner H, Wang Z, Reinscheid R;

XX WPI: 2002-383195/41.

XX N-PSDB; ABK50286.

XX Identifying an agonist, antagonist or ligand of an ADP-glucose
PT receptor, for treating cardiovascular, gastrointestinal, kidney,
PT endocrine, immune disorders, and bacterial, viral, protozoal or fungal
PT infections

XX Claim 3; Fig 1; 86pp; English.

XX The invention relates to identifying an ADP-glucose (ADP-G) receptor (a
CC G protein-coupled receptor) agonist, antagonist or ligand, comprises
CC contacting the receptor with one or more candidate compounds so that the
CC receptor produces a G protein-coupled signal in response to ADP-G or
CC selectively binds ADP-G, and identifying the candidate molecule that
CC alters signal production as an agonist, antagonist or binds as a ligand.
CC Also included are altering signalling through an ADP-G receptor, by
CC contacting a cell expressing the receptor with ADP-G or the ant/agonist,
CC ameliorating an ADP-G receptor associated condition, by administering a
CC therapeutic composition comprising ADP-G or the ant/agonist to an
CC individual and a composition comprising the ADP-G receptor and ADP-G.
CC ADP-G or the ant/agonist is useful for treating an ADP-G receptor
CC associated condition e.g. cardiovascular function disorder, where the
CC therapeutic composition induces vasorelaxation. The new methods are
CC useful in identifying ant/agonists and ligands of the receptor.

XX The ant/agonists are useful therapeutically for preventing or
CC ameliorating conditions associated with the receptor such as
CC cardiovascular disorders (e.g. ischaemia, hypertension, hypotension,
CC angina pectoris, myocardial infarction, stroke, congestive heart
CC failure, shock, erectile dysfunction, orthostatic intolerance and
CC migraine), gastrointestinal disorders (e.g. diarrhoea, gastritis,
CC inflammatory bowel disease), immune disorders (e.g. immunodeficiency
CC disorders, autoimmune disorders, rheumatoid arthritis), infections
CC caused by bacteria, fungi, protozoa or virus, respiratory disorders
CC (e.g. asthma, pneumonia, bronchitis), kidney disorders (e.g.

CC glomerulonephritis, renal failure, lupus), hepatobiliary disorders
CC (e.g. jaundice, cirrhosis, hepatitis), endocrine disorders (e.g.
CC pituitary, thyroid or adrenal dysfunctions), musculoskeletal disorders
CC (e.g. osteoporosis, muscular dystrophies), nervous system disorders
CC (e.g. Parkinson's and Alzheimer's disease), psychotic disorders (e.g.
CC depression, anxiety, schizophrenia), pain, glycogen storage
CC diseases and disorders of body weight (e.g. as a result of cancer
CC or AIDS, acquired immunodeficiency syndrome). The gene for the ADP-G
CC receptor is located on chromosome 3 in a region associated with Usher
CC syndrome type 3 (progressive hearing loss). The ligand is useful
CC therapeutically, in detecting normal or abnormal expression of the
CC receptor in an isolated sample or in in vivo diagnostic imaging
CC procedures, and targeting specifically a diagnostic group to cells and
CC tissues that express the receptor. The present sequence represents the
CC ADP-G receptor.

XX Sequence 342 AA:

Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
DB 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
QY 61 IFLKNTVISDLMLITLFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
DB 61 IFLKNTVISDLMLITLFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
QY 121 DRYQKTRPFKTSNPKNLGAKILSVIWAEMFLLSLPMLITNPNRDKNNKCSFLKS 180
DB 121 DRYQKTRPFKTSNPKNLGAKILSVIWAEMFLLSLPMLITNPNRDKNNKCSFLKS 180
QY 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
DB 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
QY 241 IIAVFICFVPHFARIPYTLTSQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPIFYFF 300
DB 241 IIAVFICFVPHFARIPYTLTSQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPIFYFF 300
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342

RESULT 9

AA048353
ID AA048353 standard; Protein: 342 AA.

AC AA048353;

DT 25-APR-2002 (first entry)

XX Human G protein-coupled receptor, IGPCR17.

XX Human: G protein-coupled receptor; IGPCR17; analgesic; neuroleptic;
XX trianquilliser; antiParkinsonian; neuroprotective; antitropic;
XX anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;
XX antidirrhoeic; osteopathic; antiallergic; antiallergic; antiallergic;
XX immunosuppressive; gene therapy; psychiatric disorder;
XX central nervous system disorder; movement dysfunction; schizophrenia;
XX multiple sclerosis; Alzheimer's disease; kidney disease; obesity;
XX gastrointestinal disorder; osteoporosis; infection;
XX gynecological disorder; receptor.

OS Homo sapiens.

XX WO200202599-A2.

XX 10-JAN-2002.

PF 02-JUL-2001; 2001WO-EP07532.

XX 30-JUN-2000; 2000US-215759P.

XX (INE-) INGENIUM PHARM AG.

PI Wattler F, Wattler S, Trommler P, Nehls MC;

XX WPI: 2002-140080/718.

DR N-PSDB; ABA96535.

PT New human or mouse G protein-coupled receptor protein, IGPCR17, useful
PT for diagnosis, prevention, amelioration or treatment of central nervous
PT system disorders such as Tourette's syndrome, Parkinson's disease and
PT pain.

XX Claim 8: Fig 2; 71pp: English.

XX The present sequence is the protein sequence for human G protein-coupled
CC receptor (GPCR) protein, IGPCR17. The coding sequence for IGPCR17 is
CC useful in gene therapy for prevention, amelioration or treatment of
CC diseases characterised by aberrant expression or activity of IGPCR17,
CC where the disease is a psychiatric or central nervous system (CNS)
CC disorder associated with signal processing in CNS such as learning and
CC memory disorders, movement dysfunctions, tics, tremor, Tourette's
CC syndrome, Parkinson's disease, Huntington's disease, dyskinesias,
CC dystonia, pain and spasms. In addition, IGPCR17 and its coding sequence
CC are useful in diagnosis, prevention, amelioration or treatment of
CC diseases associated with signal processing in CNS, schizophrenia,
CC episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive
CC disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia,
CC anorexia, kidney diseases such as renal failure, obesity,
CC gastrointestinal disorders such as irritable bowel syndrome (IBS),
CC diarrhoea, motility disorders and conditions of delayed gastric emptying,
CC osteoporosis, infections such as bacterial, fungal, protozoal and viral
CC infections, asthma, allergy, arthritis, sepsis and gynecological
CC disorders.

XX Sequence 342 AA:

Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
DB 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
QY 61 IFLKNTVISDLMLITLFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
DB 61 IFLKNTVISDLMLITLFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
QY 121 DRYQKTRPFKTSNPKNLGAKILSVIWAEMFLLSLPMLITNPNRDKNNKCSFLKS 180
DB 121 DRYQKTRPFKTSNPKNLGAKILSVIWAEMFLLSLPMLITNPNRDKNNKCSFLKS 180
QY 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
DB 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
QY 241 IIAVFICFVPHFARIPYTLTSQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPIFYFF 300
DB 241 IIAVFICFVPHFARIPYTLTSQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPIFYFF 300
QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342

RESULT 10

ABB05031
ID ABB05031 standard; Protein: 342 AA.

```

AC  ABB05031;
XX
XX  25-MAR-2002 (first entry)
XX
DE  Human SP168 receptor protein SEQ ID NO:2.
XX
XX  Human, SP168 receptor; mammalian G-Protein coupled receptor; GPCR;
XX  neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
XX  Huntington's disease; amyotrophic lateral sclerosis; ALS; MS; receptor;
XX  multiple sclerosis.
XX
OS  Homo sapiens.
XX
XX  US2001046497-A1.
XX
XX  29-NOV-2001.
XX
XX  16-APR-2001; 2001US-0835922.
XX
XX  21-APR-2000; 2000US-199041P.
XX
XX  (ZHANG/) ZHANG F L.
XX  (LHOL/) LUO L.
XX  (GUST/) GUSTAFSON E.
XX  (LIU/) LIU Y.
XX  (CHEN/) CHEN G.
XX
XX  Zhang FL, Luo L, Gustafson E, Liu Y, Chen G;
XX
XX  WPI: 2002-082414/11.
XX  N-PSDB: ABA92641.
XX
XX  Identifying modulators of mammalian G-Protein Coupled Receptor SP168,
XX  useful for treating Parkinson's Disease, Alzheimer's Disease,
XX  Huntington's Disease, amyotrophic lateral sclerosis and multiple
XX  sclerosis
XX
XX  Claim 3; Page 14-15; 16pp; English.
XX
XX  The present invention describes a method for identifying agonists and
XX  antagonists of mammalian G-Protein Coupled Receptor (GPCR) SP168 which
XX  may be used to treat neurodegenerative disorders. The method comprises:
XX  (a) contacting a mammalian SP168 receptor (or a functional fragment) in
XX  the presence of a known amount of a labeled SP168 receptor ligand with
XX  a sample to be tested for the presence of the SP168 receptor agonist or
XX  antagonist; and (b) measuring the amount of labeled SP168 ligand
XX  specifically bound to the receptor (the SP168 receptor agonist or
XX  antagonist in the sample is identified by measuring the difference in
XX  binding of the labeled SP168 receptor ligand to the receptor, compared
XX  to what would be measured in the absence of such agonist or antagonist).
XX  The method is used to detect agonists and antagonists (especially
XX  antibodies) of the SP168 GPCR which may be used to treat a
XX  neurodegenerative disorder, such as Parkinson's Disease, Alzheimer's
XX  Disease, Huntington's Disease, amyotrophic lateral sclerosis (ALS) and
XX  multiple sclerosis (MS) in mammals, especially humans. The present
XX  sequence represents the human SP168 receptor which can be used in the
XX  method of the invention.
XX
SQ  Sequence 342 AA;
Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 MQAVDNLTSAAGNTSLCTRDYKITQVLPFLLYTVLFEVGLITNGIAMRIFQIRSKSNFI 60
DB  1 MQAVDNLTSAAGNTSLCTRDYKITQVLPFLLYTVLFEVGLITNGIAMRIFQIRSKSNFI 60
OY  61 IFLKNTVISDLMLITFEFKILSDAKLGTGRLRTFVCQVTSVIFYFTYISISFLGLITI 120
DB  61 IFLKNTVISDLMLITFEFKILSDAKLGTGRLRTFVCQVTSVIFYFTYISISFLGLITI 120
OY  121 DRYOKTRPFKTSNPKNLGAKILSVIWMFLLSLPMLITNRQPRDKNVKCSFLKS 180

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DB  121 DRYOKTRPFKTSNPKNLGAKILSVIWMFLLSLPMLITNRQPRDKNVKCSFLKS 180
OY  181 EFGIWMHEIVNYICOVIMINFLIYVCYTLITELYSYRFGVGVPRKYNVAFI 240
DB  181 EFGIWMHEIVNYICOVIMINFLIYVCYTLITELYSYRFGVGVPRKYNVAFI 240
OY  241 IIAVEFICFVPHFARIPYTLISQTRDVEDCAENTLFPYKKESTLMLSLNACLDPEIFYF 300
DB  241 IIAVEFICFVPHFARIPYTLISQTRDVEDCAENTLFPYKKESTLMLSLNACLDPEIFYF 300
OY  301 LCKSFRNLSIMLKCPNSATSLSDNKRKEDGCDPNEETPM 342
DB  301 LCKSFRNLSIMLKCPNSATSLSDNKRKEDGCDPNEETPM 342

RESULT 11
AAG80236
ID  AAG80236 standard; Protein; 342 AA.
XX
XX  AAG80236;
XX
XX  24-JAN-2002 (first entry)
XX
XX  Human PAFR3 protein.
XX
XX  PAFR-3; platelet activating factor receptor; human; chromosome 3;
XX  thrombocyte activation; hypotension; vascular permeability;
XX  bronchoconstriction; transgenic animal; knockout animal.
XX
XX  Homo sapiens.
XX
XX  DE10020073-A1.
XX
XX  25-OCT-2001.
XX
XX  22-APR-2000; 2000DE-1020073.
XX
XX  22-APR-2000; 2000DE-1020073.
XX
XX  (BRUE/) BRUESS M.
XX  (BOEN/) BOENISCH H.
XX
XX  Bruess M, Boenisch H;
XX
XX  WPI: 2002-027296/04.
XX  N-PSDB: AAI68802, AAI68803.
XX
XX  New human platelet-activating factor (PAF) receptor-3 gene, useful for
XX  diagnosis and treatment of PAF-related diseases
XX
XX  Disclosure; Page 4; 6pp; German.
XX
XX  This invention describes a novel human platelet-activating factor (PAF)
XX  receptor-3 (PAFR-3) gene (I). The protein encoded by (I) probably
XX  modulates the activity of PAF, which is involved in many
XX  (patho)physiological processes, e.g., thrombocyte activation,
XX  hypotension, increased vascular permeability, bronchoconstriction etc.
XX  (I), and derived (anti)sense oligonucleotides, are useful in the
XX  treatment and diagnosis of (I)-related diseases; for producing
XX  transgenic/knockout animals, and for recombinant expression of the
XX  protein (II) that it encodes. (II) is useful in ligand-binding studies
XX  and screening assays, also for treatment and diagnosis of (II)-related
XX  diseases. This sequence represents the human platelet-activating
XX  factor receptor (PAFR-3) protein described in the invention.
XX
SQ  Sequence 342 AA;
Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 MQAVDNLTSAAGNTSLCTRDYKITQVLPFLLYTVLFEVGLITNGIAMRIFQIRSKSNFI 60

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|||||
Db 1 MQAVDNLSAGNLSLCTRDYKTIQVLEPPLYTVLFFVGLITNGLAMKIFQIRKSNFI 60
QY 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFGLITI 120
Db 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFGLITI 120
QY 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDRKNVKCSFLKS 180
Db 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDRKNVKCSFLKS 180
QY 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVAVKFI 240
Db 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVAVKFI 240
QY 241 IIAVFICFVFPFHARIPYTLISQTRDVPDCAENTLFFVKESTLMLTSLNCLDPFIYFF 300
Db 241 IIAVFICFVFPFHARIPYTLISQTRDVPDCAENTLFFVKESTLMLTSLNCLDPFIYFF 300
QY 301 LCKSFRNSLSMLKCPNSATSLSDNRRKKEDGGDPNEETPM 342
Db 301 LCKSFRNSLSMLKCPNSATSLSDNRRKKEDGGDPNEETPM 342

RESULT 12
AAI94445
ID AAY94445 standard; Protein; 342 AA.
XX
AC AAY94445;
XX
DT 21-AUG-2000 (first entry)
XX
DE Macaque ortholog of human 15625 receptor protein.
XX
KW Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
KW glial cells; spleen; colon; liver; brain; T-cell; heart;
KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
XX
OS Macaca sp.
XX
PN WO200028028-A1.
XX
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US25956.
XX
PR 06-NOV-1998; 98US-0187134.
PR 25-AUG-1999; 99US-0382918.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gluckemann MA, Gu W, Welch NS;
XX
DR WPI: 2000-376543/32.
DR N-PSDB: AAA27127.
XX
PT Identifying an agent modulating the level or activity of G-protein
PT coupled receptor useful for screening a cell derived from a subject
PT having disorders such as anaemia, neutropenia and thrombocytopenia
XX
PS Disclosure; Page 90-92; 97pp; English.
XX
CC The 15625 receptor protein is a novel G-coupled protein receptor (GPCR).
CC The cDNA for this protein was isolated by screening a human cDNA library
CC with sequences homologous to other GPCRs. The 15625 receptor protein is
CC expressed in the glial cells of the brain. It is also expressed in
CC several other tissues. The 15625 receptor protein may be useful for
CC producing antibodies which can be used to detect the presence of the
CC receptor protein. The 15625 receptor protein polynucleotides are useful
CC for generating probes, primers and antisense constructs. The
CC polynucleotides encoding the 15625 receptor proteins can also be inserted
CC into vectors to be used in gene therapy. The disorder that may be
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CC treated using the 15625 receptor protein polynucleotides and
CC polypeptides include anaemia, neutropenia and thrombocytopenia. The
CC present sequence is the macaque ortholog of the human 15625 receptor
CC protein.
CC
SQ Sequence 342 AA;
Query Match 98.3%; Score 1748; DB 21; Length 342;
Best Local Similarity 98.0%; Pred. No. 1e-183;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MQAVDNLSAGNLSLCTRDYKTIQVLEPPLYTVLFFVGLITNGLAMKIFQIRKSNFI 60
Db 1 MQAVDNLSAGNLSLCTRDYKTIQVLEPPLYTVLFFVGLITNGLAMKIFQIRKSNFI 60
QY 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFGLITI 120
Db 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFGLITI 120
QY 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDRKNVKCSFLKS 180
Db 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDRKNVKCSFLKS 180
QY 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVAVKFI 240
Db 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVAVKFI 240
QY 241 IIAVFICFVFPFHARIPYTLISQTRDVPDCAENTLFFVKESTLMLTSLNCLDPFIYFF 300
Db 241 IIAVFICFVFPFHARIPYTLISQTRDVPDCAENTLFFVKESTLMLTSLNCLDPFIYFF 300
QY 301 LCKSFRNSLSMLKCPNSATSLSDNRRKKEDGGDPNEETPM 342
Db 301 LCKSFRNSLSMLKCPNSATSLSDNRRKKEDGGDPNEETPM 342

RESULT 13
AAE04385
ID AAE04385 standard; Protein; 315 AA.
XX
AC AAE04385;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human P2-purinegic receptor subtype, P2Y12 protein fragment.
XX
KW Human; P2-purinegic receptor; P2Y12; cardiant; vasotropic; thrombolytic;
KW cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
KW myocardial infarction; ischaemic attack; pre-eclampsia; bleeding disorder;
KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
KW vascular injury; schizophrenia; eating disorder; depression; angioplasty;
KW peripheral vascular disease; platelet aggregation; restenosis; embolism;
KW thrombocytopenic purpura; stroke; perussis toxin-sensitive G protein;
KW GI; disseminated intravascular coagulation; thrombosis.
XX
OS Homo sapiens.
XX
PN WO200146454-A1.
XX
PD 28-JUN-2001.
XX
PF 26-DEC-2000; 2000WO-US34998.
XX
PR 23-DEC-1999; 99US-0171622.
XX
PA (CORT-) COR THERAPEUTICS INC.
XX
PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
PI Holloper G;
XX
DR WPI: 2001-418082/44.
DR N-PSDB: AAD08694.
XX
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PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
PT for identifying binding partners and for diagnostic applications -
XX
PS Example 1; Page 84-85; 108pp; English.
XX
CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
CC the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
CC selectively in the platelets and brain, and couples to a pertussis toxin-
CC sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
CC that responds to ADP. The invention also relates to a method for
CC identifying an agent which is useful for modulating acute myocardial
CC infarction, unstable angina, chronic stable angina, transient ischaemic
CC attacks, strokes, peripheral vascular disease, pre-eclampsia, deep venous
CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
CC thrombocytopenic purpura or a bleeding disorder: thrombotic and
CC stenotic complications following angioplasty, carotid endarterectomy,
CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
CC stent placements or insertion of endovascular devices and prostheses.
CC P2Y12 receptor is useful for identifying binding partners and for
CC diagnostic applications. P2Y12 receptor provides targets for screening
CC synthetic small molecules and combinatorial or naturally occurring
CC compound libraries to regulate platelet aggregation, vascular injury, or
CC disease as well as schizophrenia, eating disorders, depression, migraine
CC and other brain disorders. The present sequence is a fragment of human
CC P2-purinergic receptor subtype, referred as P2Y12.
XX
SQ Sequence 315 AA:
Query Match 91.9%; Score 1634; DB 22; Length 315;
Best Local Similarity 100.0%; Pred. No. 3.2e-171;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQADVNTLSAPGNTSLCTRDYKITQVLFPLLYTVLFVGLITNGLAMRIFFQIRSKSNFI 60
DB 1 MQADVNTLSAPGNTSLCTRDYKITQVLFPLLYTVLFVGLITNGLAMRIFFQIRSKSNFI 60
QY 61 IFLKNVYISDLMLTTPFKILSDAKLGTGPLRFVCOVSVIYFTWYISISFLGLITI 120
DB 61 IFLKNVYISDLMLTTPFKILSDAKLGTGPLRFVCOVSVIYFTWYISISFLGLITI 120
QY 121 DRYQKTRPFTSNPKMLLGAKLISVYIMAFMLISLPMMLTNRQPKDKVKKCSFLKS 180
DB 121 DRYQKTRPFTSNPKMLLGAKLISVYIMAFMLISLPMMLTNRQPKDKVKKCSFLKS 180
QY 181 EFLGVMHEIYVYICQVIFWINEFLIVCYTLITKELRSYVRFGVGVPRKKVNVKFI 240
DB 181 EFLGVMHEIYVYICQVIFWINEFLIVCYTLITKELRSYVRFGVGVPRKKVNVKFI 240
QY 241 IIAVFICFPFHFARIPYTLISQTRVDFDCTAENTLFYVKESTLMTSLNACDPFIYFF 300
DB 241 IIAVFICFPFHFARIPYTLISQTRVDFDCTAENTLFYVKESTLMTSLNACDPFIYFF 300
QY 301 LCKSFRNSLSMLKC 315
DB 301 LCKSFRNSLSMLKC 315
RESULT 14
AAM48354
ID AAM48354 standard: Protein; 347 AA.
AC AAM48354;
XX
XX 25-APR-2002 (first entry)
DE Murine G protein-coupled receptor, IGPCRI7.
XX
XX Murine G protein-coupled receptor, IGPCRI7; analgesic; neuroleptic;
KM transuliser; antiparkinsonian; neuroprotective; nootropic;
KM anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;
KM antidiarrhetic; osteopathic; antiasthmatic; anti allergic; antiarthritic;
KM immunosuppressive; gene therapy; psychiatric disorder;

KM central nervous system disorder; movement dysfunction; schizophrenia;
KM multiple sclerosis; Alzheimer's disease; kidney disease; obesity;
KM gastrointestinal disorder; osteoporosis; infection;
KM gynecological disorder; receptor.
XX
OS Mus musculus.
XX
PN WO200202599-A2.
XX
PD 10-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP07532.
PE 30-JUN-2000; 2000US-215759P.
PR (INGE-) INGENIUM PHARM AG.
PA
PI Wattler F, Wattler S, Trommler P, Nehls MC;
XX
XX WPI: 2002-140080/18.
DR N-PSDB; ABA98539.
XX
PT New human or mouse G protein-coupled receptor protein, IGPCRI7, useful
PT for diagnosis, prevention, amelioration or treatment of central nervous
PT system disorders such as Tourette's syndrome, Parkinson's disease and
PT pain -
XX
XX Claim 9; Fig 6; 71pp; English.
XX
CC The present sequence is the protein sequence for murine G protein-coupled
CC receptor (GPCR) protein, IGPCRI7. The coding sequence for IGPCRI7 is
CC useful in gene therapy for prevention, amelioration or treatment of
CC diseases characterised by aberrant expression or activity of IGPCRI7,
CC where the disease is a psychiatric or central nervous system (CNS)
CC disorder associated with signal processing in CNS such as learning and
CC memory disorders, movement dysfunctions, tics, tremor, Tourette's
CC syndrome, Parkinson's disease, Huntington's disease, dyskinesias,
CC dystonia, pain and spasms. In addition, IGPCRI7 and its coding sequence
CC are useful in diagnosis, prevention, amelioration or treatment of
CC diseases associated with signal processing in CNS, schizophrenia,
CC episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive
CC disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia,
CC anorexia, kidney diseases such as renal failure, obesity,
CC gastrointestinal disorders such as irritable bowel syndrome (IBS),
CC diarrhoea, motility disorders and conditions of delayed gastric emptying,
CC osteoporosis, infections such as bacterial, fungal, protozoal and viral
CC infections, asthma, allergy, arthritis, sepsis and gynecological
CC disorders.
XX
SQ Sequence 347 AA:
Query Match 87.5%; Score 1555.5; DB 23; Length 347;
Best Local Similarity 88.7%; Pred. No. 1.6e-162;
Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;
QY 6 NLTSAPGNTSLCTRDYKITQVLFPLLYTVLFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
DB 12 NLTSPGNTSLCTRDYKITQVLFPLLYTVLFVGLITNGLAMRIFFQIRSKSNFIIFLKN 71
QY 66 TVISDLMLTTPFKILSDAKLGTGPLRFVCOVSVIYFTWYISISFLGLITIDRYQK 125
DB 72 TVISDLMLTTPFKILSDAKLGTGPLRFVCOVSVIYFTWYISISFLGLITIDRYQK 131
QY 126 TTRPFTSNPKMLLGAKLISVYIMAFMLISLPMMLTNRQPKDKVKKCSFLKSEGLV 185
DB 132 TTRPFTSNPKMLLGAKLISVYIMAFMLISLPMMLTNRQPKDKVKKCSFLKSEGLV 191
QY 186 WHEIVNYICQVIFWINEFLIVCYTLITKELRSYVRFGVGVPRKKVNVKFI 245
DB 192 WHEIVNYICQVIFWINEFLIVCYTLITKELRSYVRFGVGVPRKKVNVKFI 251
QY 246 FICFVPHFARIPYTLISQTRVDFDCTAENTLFYVKESTLMTSLNACDPFIYFLCKSF 305

Db	252	FICVPPHFAIRIPIYLTISQTRAVEDCSAENLTFFVKESTLMLTSLNACLDPIFYIFLCKSE	311
Qy	306	RNSLISMLKCPNNSATLSISODNRKKEDDGGDPNRETQM	342
Db	312	RNSLISMLKCSNS-TSTSGTKRRKGEGEPESEETPM	347
RESULT 15			
AAE04384			
ID	AAE04384	standard; Protein; 343 AA.	
AC	AAE04384;		
XX			
DT	04-SEP-2001	(first entry)	
XX			
DE	Rat P2-purinergic receptor subtype, P2Y12.		
XX			
KM	Rat; P2-purinergic receptor; P2Y12; cardiac; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina myocardial infarction; ischemic attack; preclempsia; bleeding disorder carotid endarterectomy; vascular graft surgery; brain disorder; migraine vascular injury; schizoprenia; eating disorder; depression; angiodiastly peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein; GI; disseminated intravascular coagulation; thrombosis.		
XX			
OS	Rattus norvegicus.		
PN	MO200146454-A1.		
PN	28-JUN-2001.		
PD			
XX	26-DEC-2000; 2000MO-US34998.		
PR	23-DEC-1999; 990S-0171622.		
XX			
PA	(COR-) COR THERAPEUTICS INC.		
XX			
PI	Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;		
PI	Hollopeter G;		
DR	WPI; 2001-418082/44.		
DR	N-PSDB; AAD08693.		
PT	Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications -		
XX			
PS	ClaIm 14; Page 81-82; 108pp; English.		
XX			
CC	The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin sensitive G protein (G1). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischemic attacks, strokes, peripheral vascular disease, preclempsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic thrombocytopenic purpura or a bleeding disorder; thrombotic and restenotic complications following angioplasty, carotid endarterectomy, post CABG (coronary artery bypass graft) surgery, vascular graft surgery stent placements or insertion of endovascular devices and prostheses.		
CC	P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizoprenia, eating disorders, depression, migraine and other brain disorders. The present sequence is rat P2-purinergic receptor subtype, referred as P2Y12 receptor.		
XX			
Sequence	343 AA;		

	Query Match	Best Local Similarity	86.0%;	Score 1528.5;	DB 22;	Length 343;
	Matches 293;	Conservative 17;	Mismatches 22;	Indels 5;	Gaps 1;	
QY	6	NLTSPAGNTSLCTNDYKTKITQVLEPPLLYTVLFEVGLITNGLAMRIFFQJRSKSNFIIFLKN	65			
Db	12	NTSISGTSILCSRDYKTKITQVLEPPLLYTVLFEVGLITNGLAMRIFFQJRSKSNFIIFLKN	71			
QY	66	TVISLMLILTFPPFKILSDAKLIGTPRLTFCVCQVTSVIFYFPMYISISFLGLITIDRQK	125			
Db	72	TVISLMLILTFPPFKILSDAKLAGAHLKTLVCQVTSVIFYFPMYISISFLGLITIDRYLK	131			
QY	126	TTTPEKTSNPKLGLAKLISVYVIAFMFLLSPNNILINBOPRDKNVKCSFLKSEFGVY	185			
Db	132	TTTPEKTSNPKLGLAKLISVYVIAFMFLLSPNNILINRRKDKDITKCSFLKSEFGVY	191			
QY	186	WHEIYNYICQVYFWINFLIVCYTLIRKELRSYVVRTGCVGVPRKKNVAVFIIIAVF	245			
Db	192	WHEIYNYICQVYFWINFLIVCYSLIRKELRSYVVRGSKAKKRNINIVFIIIAVF	251			
QY	246	FICFVPPFHPARIPLYLSOTRDVFDCTAENLTFYKESLTLMTLSLNACLDPFIYFLCKSF	305			
Db	252	FICFVPPFHPARIPLYLSOTRAVFDENANENLTFYVESLTLMTLSLNACLDPFIYFLCKSF	311			
QY	306	RNSLISMLKCPNSATSLSDNRKKKQDGDGDPDEEPRM	342			
Db	312	RNSLISMLKRC-----STSGANKKKKQEGGDDBEEPRM	343			

Search completed: December 6, 2002, 10:06:09
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:13 ; Search time 14 Seconds

(without alignments)
718,760 Million cell updates/sec

Title: US-09-835-922-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNRRKKEODGDPNEETPM 342

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents.AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	342	3	US-08-852-824-2
2	823	46.3	333	4	US-09-221-456-2
3	823	46.3	333	4	US-09-558-740-2
4	797	44.8	333	2	US-08-812-871-1
5	772	43.4	325	2	US-08-467-948A-29
6	772	43.4	325	3	US-08-467-947A-29
7	772	43.4	338	3	US-08-988-876-8
8	772	43.4	338	4	US-09-303-524A-2
9	679.5	38.2	358	3	US-08-988-876-3
10	546.5	30.7	293	2	US-08-467-948A-6
11	546.5	30.7	293	3	US-08-467-947A-6
12	488	27.4	319	1	US-08-702-344-28
13	410.5	23.1	326	1	US-08-118-270-39
14	410.5	23.1	326	5	PCT-US93-08528-39
15	392.5	22.1	342	3	US-08-988-876-9
16	379.5	21.3	361	1	US-08-383-750-4
17	379.5	21.3	361	3	US-08-352-678-4
18	379.5	21.3	361	5	PCT-US93-09636-4
19	376	21.1	348	3	US-08-852-824-17
20	374.5	21.1	381	1	US-08-467-125-2
21	374.5	21.1	381	2	US-08-911-320A-2
22	374.5	21.1	381	4	US-09-217-101-2
23	349.5	19.7	302	2	US-08-467-948A-30
24	349.5	19.7	302	3	US-08-467-947A-30
25	339	19.1	344	2	US-08-467-948A-8
26	339	19.1	344	3	US-08-467-947A-8
27	337	19.0	68	4	US-08-905-223-327

28	329.5	18.5	339	1	US-08-153-848-44	Sequence 44, Appl
29	329.5	18.5	339	2	US-08-812-871-3	Sequence 3, Appl1
30	329.5	18.5	339	3	US-09-299-843A-44	Sequence 44, Appl
31	329.5	18.5	339	4	US-08-088-337B-44	Sequence 44, Appl
32	329.5	18.5	339	5	PCT-US93-11153-44	Sequence 44, Appl
33	329.5	18.5	339	5	PCT-US95-07180-2	Sequence 2, Appl1
34	329	18.5	359	1	US-08-041-219A-6	Sequence 6, Appl1
35	329	18.5	359	1	US-08-417-122-6	Sequence 6, Appl1
36	327.5	18.4	395	1	US-08-097-938-2	Sequence 2, Appl1
37	327.5	18.4	395	1	US-08-476-000-2	Sequence 2, Appl1
38	327.5	18.4	395	2	US-08-472-840-2	Sequence 2, Appl1
39	327.5	18.4	395	2	US-08-476-976-2	Sequence 2, Appl1
40	327.5	18.4	395	3	US-08-474-410-2	Sequence 2, Appl1
41	325.5	18.3	395	4	US-08-486-673B-2	Sequence 2, Appl1
42	325.5	18.3	395	4	US-08-486-673B-5	Sequence 5, Appl1
43	325.5	18.3	399	1	US-08-476-000-61	Sequence 61, Appl
44	325.5	18.3	399	1	US-08-472-840-61	Sequence 61, Appl
45	325.5	18.3	399	2	US-08-476-976-61	Sequence 61, Appl

ALIGNMENTS

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RESULT 1
US-08-852-824-2
; Sequence 2, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: IJ et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.122000
; CURRENT APPLICATION NUMBER: US/08/852,824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: genomic
US-08-852-824-2

Query Match      100.0%; Score 1778; DB 3; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.9e+144;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKITQVLPPLTYLFFVGLITNGLAMRIFFOIRSKNFI 60
DB 1 MQAVDNLTSAPGNTSLCTRDYKITQVLPPLTYLFFVGLITNGLAMRIFFOIRSKNFI 60
QY 61 IFLKNTVISDLMLITLFPFKIISDAKLTGTPLTFCQVTSVIFYFTWYISIFGLITI 120
DB 61 IFLKNTVISDLMLITLFPFKIISDAKLTGTPLTFCQVTSVIFYFTWYISIFGLITI 120
QY 121 DRYOKTRPFKSNPKNLGAKILSVYIAPMFLSLPMIITLNROPDKNNKCSFLKS 180
DB 121 DRYOKTRPFKSNPKNLGAKILSVYIAPMFLSLPMIITLNROPDKNNKCSFLKS 180
QY 121 DRYOKTRPFKSNPKNLGAKILSVYIAPMFLSLPMIITLNROPDKNNKCSFLKS 180
DB 121 DRYOKTRPFKSNPKNLGAKILSVYIAPMFLSLPMIITLNROPDKNNKCSFLKS 180
QY 181 ERLVHEIYNTICQVIFWIFNLIVCYTLTKELYSYVRGKVPKKNVKNVKT 240
DB 181 ERLVHEIYNTICQVIFWIFNLIVCYTLTKELYSYVRGKVPKKNVKNVKT 240
QY 241 IIAVFICVPHFARIPYTLISQTRDVPDCTAENTLFYVKESTLMTSLNACIDPIYTF 300
DB 241 IIAVFICVPHFARIPYTLISQTRDVPDCTAENTLFYVKESTLMTSLNACIDPIYTF 300
QY 301 LCKSFNLSISMCKCPNSATLSQDNRRKKEODGDPNEETPM 342
DB 301 LCKSFNLSISMCKCPNSATLSQDNRRKKEODGDPNEETPM 342
; RESULT 2
; US-09-221-456-2
; Sequence 2, Application US/09221456
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; Patent No. 6162899
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERES, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEA81 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestla
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,456
; FILING DATE: 28-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,975
; FILING DATE: 23-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestla, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-221-456-2

Query Match          46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 5,9e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;
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RESULT 3
US-09-558-740-2
; Sequence 2, Application US/09558740
; Patent No. 6358695
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERES, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE HNEA81 RECEPTOR
; FILE REFERENCE: GH-70318-2
; CURRENT APPLICATION NUMBER: US/09/558,740
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 08/956,975
; PRIOR FILING DATE: 1997-10-23
; PRIOR APPLICATION NUMBER: 09/221,456
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-558-740-2

Query Match          46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 5,9e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;
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STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812.871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MBLR3DT01
CLONE: 568987
US-08-812-871-1

Query Match          44.8%; Score 797; DB 2; Length 333;
Best Local Similarity 47.8%; Pred. No. 9.8e-61;
Matches 151; Conservative 57; Mismatches 106; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLEPLLTYLVFVGLITNGLARIFQIRSKSNFIIFLKNVISDLMILT 76
DB 15 CPRDRIQVLPALYVFLTGILNLTALWVFIHPSSTFIYKNTLVADLIMLTLM 74
QY 77 FPEKLSDAKLGTPGRFVQVTSVIFFTMYISISFLGTTIDRYOKTTPEFKTSNK 136
DB 75 LPEKLSDAKLGTPGRFVQVTSVIFFTMYISISFLGTTIDRYOKTTPEFKTSNK 134
QY 137 NLGAKIISVVAWFMFLSLPNMILITNRQPRDKNVKCSFLKSEGLVWHEIVNYICOV 196
DB 135 KPVFAKTVSIFLWFLFISLPIMLSNKEATPSSVKKCASLKGPLGLKMHQMVNNICOF 194
QY 197 IFWIFLIVCYTLITRELYRSYVTRGVGKVPKRVNVKVIIVAFICFVPHFAR 256
DB 195 IFWVLIILMLVYVIAKVVDSYRSKCKDKRNKKNKLEGKVVVVVAVFVFCFAPFHAR 254
QY 257 IPTYISQTRDVFDCYAEVNTLFYKVESTIMLTSLNACDPIFYFLCKSRNLSIMLKP 316
DB 255 VPTYISQTRDVFDCYAEVNTLFYKVESTIMLTSLNACDPIFYFLCKSRNLSIMLKP 312
QY 317 NSATSLSDNRKKEOD 332
DB 313 RKTASSQENHSSQTD 328

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RESULT 5
US-08-467-948A-29
Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:

APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.

```

APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor CPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

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Query Match 43.4%; Score 772; DB 2; Length 325;
Best Local Similarity 47.5%; Pred. No. 1.3e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

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QY 6 NLTSAPAGNTSLCTRDYKIQVLEPLLTYLVFVGLITNGLARIFQIRSKSNFIIFLKN 65
DB 2 NSTSQPPDESQSNLITQIIPVLCVWFIAGILNAGVSGWIFVYVSSSFIIYKLN 61
QY 66 TVISDLMITLTPFKILSDAKLGTPGRFVQVTSVIFFTMYISISFLGTTIDRYOK 125
DB 62 IVIADFVMSLTPFKILSDGSGIPQNLVFCVSAVLEFVNMVYSIVFFGLISFDRYK 121
QY 126 TTRPRTSNPKLNLAKIISVVAWFMFLSLPNMILITNRQPRDKNVKCSFLKSEFLV 185
DB 122 IYKPLMTSFTQSVYSKLSLVYMMILMLAVNIIITNQSVREYQICELKSELGK 181
QY 186 WHEIYNYICOVFWIFLIVCYTLITRELYRSYVTRGVGKVPKRVNVKVIIVAFI 245
DB 182 WHKASNYIFVALFWIFLIVCYTLITRELYRSYVTRGVGKVPKRVNVKVIIVAFI 241
QY 246 FICFVPHFARIPYTLISQTRDVFDCYAEVNTLFYKVESTIMLTSLNACDPIFYFLCK 305
DB 242 FVCFVPHFARIPYTLISQTRDVFDCYAEVNTLFYKVESTIMLTSLNACDPIFYFLCK 301
QY 306 RNSLSMLKCPNSA 319
DB 302 REILCKKLIHPLKA 315

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RESULT 6
US-08-467-947A-29
Sequence 29, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:

Patent No 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULL, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein


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1038
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[illegible]

```

1      RESULT 15
2      US-08-988-876-9
3      : Sequence 9, Application US/08988876
4      : Patent No. 6063596
5      : GENERAL INFORMATION:
6      :   APPLICANT: Lal, Preeti
7      :   APPLICANT: Bandman, Olga
8      :   APPLICANT: Hillman, Jennifer L.
9      :   APPLICANT: Yue, Henry
10     : TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
11     : TITLE OF INVENTION: WITH IMMUNE RESPONSE
12     : NUMBER OF SEQUENCES: 9
13     : CORRESPONDENCE ADDRESS:
14     :   ADDRESSEE: Incyte Pharmaceuticals, Inc.
15     :   STREET: 3174 Porter Drive
16     :   CITY: Palo Alto
17     :   STATE: CA
18     :   COUNTRY: USA
19     :   ZIP: 94304
20     : COMPUTER READABLE FORM:
21     :   MEDIUM TYPE: Diskette
22     :   COMPUTER: IBM Compatible
23     :   OPERATING SYSTEM: DOS
24     :   SOFTWARE: FastSeq for Windows Version 2.0
25     :   CURRENT APPLICATION DATA:
26     :     APPLICATION NUMBER: US/08/988,876
27     :     FILING DATE: Herewith
28     :   CLASSIFICATION:
29     :     PRIOR APPLICATION DATA:
30     :       APPLICATION NUMBER:
31     :     FILING DATE:
32     :   ATTORNEY/AGENT INFORMATION:
33     :     NAME: Billings, Lucy J.
34     :     REGISTRATION NUMBER: 36,749
35     :     REFERENCE/DOCKET NUMBER: PF-0441 US
36     :     TELECOMMUNICATION INFORMATION:
37     :       TELEPHONE: 650-855-0555
38     :       TELEFAX: 650-845-4166
39     :     TELEX:
40     :   INFORMATION FOR SEQ ID NO: 9:
41     :     SEQUENCE CHARACTERISTICS:
42     :       LENGTH: 342 amino acids
43     :       TYPE: amino acid
44     :       STRANDEDNESS: single
45     :       TOPOLOGY: linear
46     :     IMMEDIATE SOURCE:
47     :       LIBRARY: Genbank
48     :       CLONE: 49443
49     :   US-08-988-876-9

```

[illegible]

Db 243 ICFVPHHVOIPWTLAEI-GMFPSSNHQAINDAHQVITICLLSTNCVLDPVITCYCFLTKKR 301
QY 307 NSLISM LKCPNSATSLSQDNRRKEQGGDPNEETPM 342
Db 302 KHLSEKLNIMRSSQKCSRVTDTGTGEMAIPIINHTEPV 337

Search completed: December 6, 2002, 10:08:19
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2002, 10:06:15 ; Search time 119 Seconds
(without alignments)
46.680 Million cell updates/sec

Title: US-09-835-922-2
Perfect score: 1778
Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SDNRKKKEQDGDPNETPM 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```

1: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB pep: *
2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB pep: *
3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB pep: *
4: /cgn2_6/ptodata/1/pubpa/US06_PUBCOMB pep: *
5: /cgn2_6/ptodata/1/pubpa/US07_NEW_PUB pep: *
6: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB pep: *
7: /cgn2_6/ptodata/1/pubpa/PCTUS_PUBCOMB pep: *
8: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB pep: *
9: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUB pep: *
10: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB pep: *
11: /cgn2_6/ptodata/1/pubpa/US10_NEW_PUB pep: *
12: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB pep: *
13: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB pep: *
14: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB pep: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1778	100.0	342	9	US-09-964-008-1	Sequence 1, Appl
2	1778	100.0	342	10	US-09-835-922-2	Sequence 2, Appl
3	1778	100.0	342	10	US-09-827-937A-2	Sequence 2, Appl
4	1778	100.0	342	10	US-09-780-576-2	Sequence 2, Appl
5	1748	98.3	342	9	US-09-964-008-3	Sequence 3, Appl
6	823	46.3	333	10	US-09-769-159-2	Sequence 2, Appl
7	797	44.8	333	10	US-09-848-889-1	Sequence 1, Appl
8	772	43.4	338	10	US-09-919-497-77	Sequence 77, Appl
9	741.5	41.7	338	10	US-09-826-508-20	Sequence 20, Appl
10	694.5	39.1	358	10	US-09-826-508-10	Sequence 10, Appl
11	679.5	38.2	358	9	US-09-974-298-86	Sequence 86, Appl
12	679.5	38.2	358	10	US-09-919-172-22	Sequence 22, Appl
13	488	27.4	319	12	US-10-025-335-1	Sequence 1, Appl
14	385	21.7	327	12	US-10-084-206-3	Sequence 3, Appl
15	376	21.1	348	10	US-09-927-937A-17	Sequence 17, Appl
16	374.5	21.1	381	10	US-09-997-532-2	Sequence 2, Appl
17	347.5	19.5	330	10	US-09-826-791-2	Sequence 2, Appl
18	347.5	19.5	346	9	US-09-828-478-6	Sequence 4, Appl
19	347.5	19.5	346	10	US-09-826-791-6	Sequence 6, Appl

ALIGNMENTS

20	347.5	19.5	346	10	US-09-866-230-7	Sequence 7, Appl1
21	347.5	19.5	346	10	US-09-866-230-9	Sequence 9, Appl1
22	334	18.8	367	9	US-09-828-478-6	Sequence 6, Appl1
23	329.5	18.5	299	9	US-09-860-670-011	Sequence 81, Appl1
24	329.5	18.5	299	10	US-09-764-653-521	Sequence 521, App
25	329.5	18.5	339	9	US-09-828-478-4	Sequence 4, Appl1
26	329.5	18.5	339	10	US-09-848-689-12	Sequence 12, Appl1
27	329.5	18.5	339	10	US-09-788-133-2	Sequence 2, Appl1
28	321	18.1	359	10	US-09-867-569-9	Sequence 9, Appl1
29	317.5	17.9	398	10	US-09-823-114-16	Sequence 16, Appl1
30	317.5	17.9	398	10	US-09-966-871-1	Sequence 1, Appl1
31	317.5	17.9	398	12	US-10-039-645-1	Sequence 1, Appl1
32	315	17.7	405	10	US-09-966-871-84	Sequence 84, Appl1
33	315	17.7	405	12	US-10-039-645-84	Sequence 84, Appl1
34	314.5	17.7	398	10	US-09-966-871-79	Sequence 79, Appl1
35	314.5	17.7	398	12	US-10-039-645-79	Sequence 79, Appl1
36	313	17.6	382	10	US-09-993-844-4	Sequence 4, Appl1
37	313	17.6	415	10	US-09-823-114-20	Sequence 20, Appl1
38	312	17.5	359	10	US-09-966-871-81	Sequence 81, Appl1
39	312	17.5	359	12	US-10-039-645-81	Sequence 81, Appl1
40	309.5	17.4	380	10	US-09-149-045-2	Sequence 2, Appl1
41	309	17.4	400	10	US-09-966-871-85	Sequence 85, Appl1
42	309	17.4	400	12	US-10-039-645-85	Sequence 85, Appl1
43	306	17.2	400	10	US-09-966-871-78	Sequence 78, Appl1
44	306	17.2	400	12	US-10-039-645-78	Sequence 78, Appl1
45	305	17.2	400	10	US-09-966-871-86	Sequence 86, Appl1

RESULT 1
US-09-964-008-1

```

: GENERAL INFORMATION:
: APPLICANT: Glucksmann, Maria A.
: APPLICANT: Gu, Wei
: TITLE OF INVENTION: 15625 Receptor, A No. US20020156246A1el G-Protein Coupled Rece
: FILE REFERENCE: 5800-13, 035800-171548
: CURRENT APPLICATION NUMBER: US/09/964,008
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/187,134
: PRIOR FILING DATE: 1998-11-06
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 1
: LENGTH: 342
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-964-008-1

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Query Match	Score	DB 9	Length
100.0%	1778	342	

QY	1	MOAVONLSAPBNTSLC	RDYK	ITOV	LEPL	LYTV	FFPGL	ITNG	LAM	LEFO	IRKS	NFI	60																					
Db	1	MOAVONLSAPBNTSLC	RDYK	ITOV	LEPL	LYTV	FFGL	ITNG	LAM	LEFO	IRKS	NFI	60																					
QY	61	IFLKNTVNSDLMIL	TFPK	ILSDAK	LGTG	PLTE	VCOT	SV	IFET	FW	IS	ISFGL	ITI	120																				
Db	61	IFLKNTVNSDLMIL	TFPK	ILSDAK	LGTG	PLTE	VCOT	SV	IFET	FW	IS	ISFGL	ITI	120																				
QY	121	DRYQTTREPKTS	SNRKNL	GAKIL	SVVI	AE	MFLL	SLP	NMIL	TNRQ	PD	RKNV	KCS	FLKS	180																			
Db	121	DRYQTTREPKTS	SNRKNL	GAKIL	SVVI	AE	MFLL	SLP	NMIL	TNRQ	PD	RKNV	KCS	FLKS	180																			
QY	181	ERGLWHELVAN	ICOV	IF	IN	FL	IV	YCT	LL	TKEL	YS	YAT	RGV	AV	PR	KV	WV	KFI	240															
Db	181	ERGLWHELVAN	ICOV	IF	IN	FL	IV	YCT	LL	TKEL	YS	YAT	RGV	AV	PR	KV	WV	KFI	240															
QY	241	IAVE	FI	CV	FP	HP	FA	RI	PT	VS	LSQ	TRD	V	ED	CT	A	EN	L	FW	K	ES	T	LW	L	TS	LN	A	C	LD	P	FI	VE	F	300
Db	241	IAVE	FI	CV	FP	HP	FA	RI	PT	VS	LSQ	TRD	V	ED	CT	A	EN	L	FW	K	ES	T	LW	L	TS	LN	A	C	LD	P	FI	VE	F	300

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Db 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLFFVKESTLMLSLNACLDPEITYFF 300
QY 301 LCKSFRNSLSMLKCPNSATSLSODNRKKEQDGDGPNEETPM 342
Db 301 LCKSFRNSLSMLKCPNSATSLSODNRKKEQDGDGPNEETPM 342

```

RESULT 2

```

US-09-835-922-2
; Sequence 2, Application US/09835922
; Patent No. US20010046497A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Fang L.
; APPLICANT: Luo, Lin
; APPLICANT: Gustafson, Eric
; APPLICANT: Liu, Yan-Hui
; APPLICANT: Chen, Guodong
; TITLE OF INVENTION: G-Protein Coupled Receptor and Methods
; FILE REFERENCE: CN01167K
; CURRENT APPLICATION NUMBER: US/09/835,922
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/199,041
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-835-922-2

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Query Match          100.0%; Score 1778; DB 10; Length 342;
Best Local Similarity 100.0%; Pred. No. 5,8e-151;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
Db 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFKNTVYISDLMLTFPPFKILSDAKLGTGPLRFTVCQVSVIFFTMYISISFLGLITI 120
Db 61 IFKNTVYISDLMLTFPPFKILSDAKLGTGPLRFTVCQVSVIFFTMYISISFLGLITI 120
QY 121 DRYQKTRPEKTSNPKNLGAKILSVIYMAFMFLSLPNNMLITNRQPRDKNVKCSFLKS 180
Db 121 DRYQKTRPEKTSNPKNLGAKILSVIYMAFMFLSLPNNMLITNRQPRDKNVKCSFLKS 180
QY 181 EFGVWHEIYVYICQVIFWINEFLIVICYTLITKELYSYVTRGVGKVPKKVNVKVEI 240
Db 181 EFGVWHEIYVYICQVIFWINEFLIVICYTLITKELYSYVTRGVGKVPKKVNVKVEI 240
QY 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLFFVKESTLMLSLNACLDPEITYFF 300
Db 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLFFVKESTLMLSLNACLDPEITYFF 300
QY 301 LCKSFRNSLSMLKCPNSATSLSODNRKKEQDGDGPNEETPM 342
Db 301 LCKSFRNSLSMLKCPNSATSLSODNRKKEQDGDGPNEETPM 342

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RESULT 3

```

US-09-827-937A-2
; Sequence 2, Application US/09827937A
; Patent No. US20020052043A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruden, Steven M.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488,1220003
; CURRENT APPLICATION NUMBER: US/09/827,937A
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 08/852,824

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; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-937A-2

```

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Query Match          100.0%; Score 1778; DB 10; Length 342;
Best Local Similarity 100.0%; Pred. No. 5,8e-151;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
Db 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFKNTVYISDLMLTFPPFKILSDAKLGTGPLRFTVCQVSVIFFTMYISISFLGLITI 120
Db 61 IFKNTVYISDLMLTFPPFKILSDAKLGTGPLRFTVCQVSVIFFTMYISISFLGLITI 120
QY 121 DRYQKTRPEKTSNPKNLGAKILSVIYMAFMFLSLPNNMLITNRQPRDKNVKCSFLKS 180
Db 121 DRYQKTRPEKTSNPKNLGAKILSVIYMAFMFLSLPNNMLITNRQPRDKNVKCSFLKS 180
QY 181 EFGVWHEIYVYICQVIFWINEFLIVICYTLITKELYSYVTRGVGKVPKKVNVKVEI 240
Db 181 EFGVWHEIYVYICQVIFWINEFLIVICYTLITKELYSYVTRGVGKVPKKVNVKVEI 240
QY 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLFFVKESTLMLSLNACLDPEITYFF 300
Db 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLFFVKESTLMLSLNACLDPEITYFF 300
QY 301 LCKSFRNSLSMLKCPNSATSLSODNRKKEQDGDGPNEETPM 342
Db 301 LCKSFRNSLSMLKCPNSATSLSODNRKKEQDGDGPNEETPM 342

```

RESULT 4

```

US-09-780-576-2
; Sequence 2, Application US/09780576
; Patent No. US20020072072A1
; GENERAL INFORMATION:
; APPLICANT: Clivelli, Olivier
; APPLICANT: Wang, Zhwei
; APPLICANT: Reinscheid, Rainer
; TITLE OF INVENTION: Adp-Glucose Receptor
; FILE REFERENCE: P-UC 4530
; CURRENT APPLICATION NUMBER: US/09/780,576
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/234,025
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-576-2

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Query Match          100.0%; Score 1778; DB 10; Length 342;
Best Local Similarity 100.0%; Pred. No. 5,8e-151;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
Db 1 MOAVDNLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFKNTVYISDLMLTFPPFKILSDAKLGTGPLRFTVCQVSVIFFTMYISISFLGLITI 120
Db 61 IFKNTVYISDLMLTFPPFKILSDAKLGTGPLRFTVCQVSVIFFTMYISISFLGLITI 120

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[illegible][illegible]


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: ORGANISM: HOMO SAPIENS
US-09-826-508-10
Query Match      39.1%; Score 694.5; DB 10; Length 358;
Best Local Similarity 42.2%; Pred. No. 1.2e-54;
Matches 139; Conservative 68; Mismatches 113; Indels 9; Gaps 5;

OY 6 NUTSAPG-NTSLCTRDYKITOVLPFLTYVLEFVGLTNGLAMRIEFOIRKSNFTIEFLK 64
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 25 NNSDGPGRKNTYL--HNEFDITVLPVLVLIIFVASILNGLAWLFEFHRNKTSTIEFLK 81
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 65 NTVISDLMLITLFPFKILSDAKLGTGRTFVCQTSVIEFTYMTISISFLGLITIDRYO 124
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 82 NIVVADLMTLTFPPRIYHDAGFGWYEFKILCRTSVLEFANMTSTIEFLGLISIDRL 141
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 125 KTRPFKTSNPKNLGAKILSVIYIAFMFLSLPMMILTNROPDRDKNVKKSFLKSEFGL 184
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 142 KVVKEFGDSRMYSITFTYVLSVCVWVIMAVLSLPMIILTNQPTDNIHDCSKLSPGLG 201
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 185 VVHEIVNYICQVIFWINEFLIVCYTLITKELYSYVTRGVKVPKR-KVAVKVFIIIA 243
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 202 KWHTAVTYVNSCLFVAVALVILIGCYIAISRYTHKS--SRQFISQSSRRKKNQSIYVVA 259
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 244 VEFICFVFPFHARIPYTLISQTRDVPDCTAENTLFEVKESTLMTLSLACLDPIIYFFLCK 303
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 260 VEFICFELPHLCRMSTSHDRLDESAOKILYYCKEITLFLSACNVCIDPIIYFFMCR 319
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 304 SFRNSLI--SMLKCPNSATSLSDNRKKE 330
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 320 SFSRRLFKKSNIRTSSESIRSIQSVRRSE 348
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11
US-09-974-298-86
: Sequence 86, Application US/09974298
: Patent No. US20020156263A1
: GENERAL INFORMATION:
: APPLICANT: Chen, Huel-Mei
: TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
: FILE REFERENCE: PA-0037 P
: CURRENT APPLICATION NUMBER: US/09/974, 298
: PRIOR FILING DATE: 2001-10-04
: PRIOR APPLICATION NUMBER: 60/238, 331
: NUMBER OF SEQ ID NOS: 194
: SOFTWARE: PERL Program
: SEQ ID NO 86
: LENGTH: 358
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No. US20020156263A1 1650519CD1
US-09-974-298-86

Query Match      38.2%; Score 679.5; DB 9; Length 358;
Best Local Similarity 43.7%; Pred. No. 2.6e-53;
Matches 132; Conservative 64; Mismatches 99; Indels 7; Gaps 4;

OY 6 NUTSAPG-NTSLCTRDYKITOVLPFLTYVLEFVGLTNGLAMRIEFOIRKSNFTIEFLK 64
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 25 NNSDGPGRKNTYL--HNEFDITVLPVLVLIIFVASILNGLAWLFEFHRNKTSTIEFLK 81
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 65 NTVISDLMLITLFPFKILSDAKLGTGRTFVCQTSVIEFTYMTISISFLGLITIDRYO 124
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 82 NIVVADLMTLTFPPRIYHDAGFGWYEFKILCRTSVLEFANMTSTIEFLGLISIDRL 141
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 125 KTRPFKTSNPKNLGAKILSVIYIAFMFLSLPMMILTNROPDRDKNVKKSFLKSEFGL 184
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 142 KVVKEFGDSRMYSITFTYVLSVCVWVIMAVLSLPMIILTNQPTDNIHDCSKLSPGLG 201
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 185 VVHEIVNYICQVIFWINEFLIVCYTLITKELYSYVTRGVKVPKR-KVAVKVFIIIA 243
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```

DB 202 KWHTAVTYVNSCLFVAVALVILIGCYIAISRYTHKS--SRQFISQSSRRKKNQSIYVVA 259
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 244 VEFICFVFPFHARIPYTLISQTRDVPDCTAENTLFEVKESTLMTLSLACLDPIIYFFLCK 303
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 260 VEFICFELPHLCRMSTSHDRLDESAOKILYYCKEITLFLSACNVCIDPIIYFFMCR 319
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 304 SF 305
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 320 SF 321
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 12
US-09-919-172-22
: Sequence 22, Application US/09919172
: Patent No. US20020119463A1
: GENERAL INFORMATION:
: APPLICANT: Fairs, Mary
: TITLE OF INVENTION: PROSTATE CANCER MARKERS
: FILE REFERENCE: PA-0036 US
: CURRENT APPLICATION NUMBER: US/09/919, 172
: PRIOR FILING DATE: 2001-07-28
: PRIOR APPLICATION NUMBER: 60/222, 469
: NUMBER OF SEQ ID NOS: 102
: SOFTWARE: PERL Program
: SEQ ID NO 22
: LENGTH: 358
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No. US20020119463A1 1650519CD1
US-09-919-172-22

Query Match      38.2%; Score 679.5; DB 10; Length 358;
Best Local Similarity 43.7%; Pred. No. 2.6e-53;
Matches 132; Conservative 64; Mismatches 99; Indels 7; Gaps 4;

OY 6 NUTSAPG-NTSLCTRDYKITOVLPFLTYVLEFVGLTNGLAMRIEFOIRKSNFTIEFLK 64
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 25 NNSDGPGRKNTYL--HNEFDITVLPVLVLIIFVASILNGLAWLFEFHRNKTSTIEFLK 81
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 65 NTVISDLMLITLFPFKILSDAKLGTGRTFVCQTSVIEFTYMTISISFLGLITIDRYO 124
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 82 NIVVADLMTLTFPPRIYHDAGFGWYEFKILCRTSVLEFANMTSTIEFLGLISIDRL 141
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 125 KTRPFKTSNPKNLGAKILSVIYIAFMFLSLPMMILTNROPDRDKNVKKSFLKSEFGL 184
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 142 KVVKEFGDSRMYSITFTYVLSVCVWVIMAVLSLPMIILTNQPTDNIHDCSKLSPGLG 201
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 185 VVHEIVNYICQVIFWINEFLIVCYTLITKELYSYVTRGVKVPKR-KVAVKVFIIIA 243
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 202 KWHTAVTYVNSCLFVAVALVILIGCYIAISRYTHKS--SRQFISQSSRRKKNQSIYVVA 259
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 244 VEFICFVFPFHARIPYTLISQTRDVPDCTAENTLFEVKESTLMTLSLACLDPIIYFFLCK 303
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 260 VEFICFELPHLCRMSTSHDRLDESAOKILYYCKEITLFLSACNVCIDPIIYFFMCR 319
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 304 SF 305
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 320 SF 321
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 13
US-10-025-335-1
: Sequence 1, Application US/10025335
: Patent No. US20020127648A1
: GENERAL INFORMATION:
: APPLICANT: Coleman, Roger
: TITLE OF INVENTION: NOVEL HUMAN C5A-LIKE RECEPTOR
: NUMBER OF SEQUENCES: 3
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/025,335
FILING DATE: 18-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,974
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0198 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 346874
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-025-335-1

Query Match      27.4%; Score 488; DB 12; Length 319;
Best Local Similarity 34.5%; Pred. No. 2,4e-36;
Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 NTSLSCTROYKITQVLFPLLYTVLFVFGVLTGNCGLAMRIFQIRSKSNFT-IFLKNTVISDL 71
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 3 NSSFCPPYKDELP-FTFEFYLVFLVGIIGSCFATWAFIQKNTNHRVCYSIYLINLTADF 61
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 72 IMILFEPKILSDAKLGTGCP-LRPFVCOVTVSIEFTMYTISISPLGLITIDRYQKTRP 129
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 62 LITLALPKRIAYVD-LGVAIPMKLKFHCQVTAACLIYINMYLSITFLAFYSIDRCLOLTHS 119
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 130 FKTSPNKMILGKILSYVIMAFMFLSLSPNMLITNROPDRKKVKKCSFLKSEGLVMEI 189
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 120 CKIYNIGQSPFKAMISTYVMVLMVLLIMYPNMKIP-IRKDIKESKNVCMERKKEFGNNHLL 179
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 190 VNYICQVIFWINE-LIVIVCYTLITLKELYRSYVTRGVGVKVP-RKVNVKVEFIITAVEFI 247
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 180 TNEICVAIF-INFSAILIISCLVIRQLYRN----KDNENYPNVKALINILLVTTGYII 234
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 248 CFVPRHFARIPTLTSQTDVDCIATENLFLFYKESTIMLTSINACLDPFIYFLCKSPRN 307
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 235 CFVPRHIVIRIPTLSQTEVITDCSIRISLFFAKKENTLLLAASNLCEFDPLLYVHLSKAFRS 294
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 308 SLI-----SMLKCPNSA 319
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 295 KYTEFFASPKETKAKOKELRCENNA 319
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 14
US-10-084-206-3
Sequence 3, Application US/10084206
Patent No. US20020106741A1
GENERAL INFORMATION:

```

APPLICANT Li et al.

TITLE OF INVENTION: G-Protein Receptor HTNAD29

FILE REFERENCE: PRI9IDIC1

CURRENT APPLICATION NUMBER: US/10/084, 206

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US95/07288

PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: 08/468, 534

PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: 09/399, 095

PRIOR FILING DATE: 1999-09-20

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 3

LENGTH: 327

TYPE: PRT

ORGANISM: Homo sapiens

US-10-084-206-3

Query Match 21.7%; Score 385; DB 12; Length 327;
Best Local Similarity 32.6%; Pred. No. 3,6e-27;

Matches 104; Conservative 57; Mismatches 134; Indels 24; Gaps 9

OY 20 DYKIQVLEPLLTYLFLFVGGLITNCILAMRIFQIR--SKSNTI-TFIKNTVISDLMILT 76
| : |::||:::||:|::| : : : : || : | : : |:|:
Db 6 DSEERYTLPPIVTSLTEFLGVATNGSYVLWVEFKRLPCKKFENIKETIMWLTMADMILEFIT 65

OY 77 EPEKLSDAKTGTPDRFYVCQTAVIFEFTWTYSISFGTLTIIRDYOKTRPPKTSNPX 136
| : |::||:::||:~::~|: ~ ::||:~:~::||:~:~::||
Db 66 LPLMTVVYQQONGNMWLLPRFLCNAVACLEFPINNYCSVAELGVTYYNRFOAVTPRKTAQN 125

OY 137 NLGALKLSVIIV---AFMFLSLPMNLITNQRPDX--NVKKCSFLKSEFGLIWHE 188
| : |::||:::||:~::~|: ~ ::||:~:~::||:~:~::||
Db 126 TRRGISTLIIVTWAIWGAAASYFLILDS--TNTPVDASGSQNWTRRC-FEHYEKGSPVYL 181

OY 189 IVANYICOVFEMINFLLIVCYLTLLKELYRSYVRGRGKVPRKRKYNAVKFFIIIAVFPC 248
| : |::||:::||:~::~|: ~ ::||:~:~::||:~:~::||
Db 182 ITHIPVSFEFLVELILLFCMLVIIITRTLMDPVGOQRNAEYGALMW-VCTVLAVFILIG 240

OY 249 VPFPHFAHPIPTLSOTRDVFDETAENTLFYVKESTIAMLITSLNACDPDFIFFLKSSFN- 307
| : |::||:::||:~::~|: ~ ::||:~:~::||:~:~::||
Db 241 FVPHHVQLDPLMTAEL-GFODSKFHQAINDAQYTLCCLSTCNVDPAVITYCELTTKFRKH 299

OY 308 -----SLISMUKCPNSAT 320
| : |::||:::||:~::~|: ~ ::||:~:~::||:~:~::||
Db 300 LTEKEYSMRSSRKCSRATT 318

RESULT 15

US-09-827-937A-17

Sequence 17, Application US/09827937A

Patent No. US20020052043A1

GENERAL INFORMATION:

APPLICANT: LI, YI

APPlicant: Ruben, Steven M.

TITLE OF INVENTION: Human G-Protein Coupled Receptors

FILE REFERENCE: 1488_1220003

CURRENT APPLICATION NUMBER: US/09/827, 937A

CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 08/852, 824

PRIOR FILING DATE: 1997-05-07

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 17

LENGTH: 348

TYPE: PRT

ORGANISM: Homo sapiens

US-09-827-937A-17

Query Match 21.1%; Score 376; DB 10; Length 348;
Best Local Similarity 26.1%; Pred. No. 2.4e-26;

Matches 94; Conservative 83; Mismatches 153; Indels 30; Gaps 11

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:11; Search time 33 Seconds

(without alignments)
429.846 Million cell updates/sec

Title: US-09-835-922-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSPGNTSLCTRD.....SQDNKKKQDGGDPNEETPM 342

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	1	P2YC_HUMAN
2	1748	98.3	342	1	P2YC_MACPA
3	1555.5	87.5	347	1	P2YC_MOUSE
4	1528.5	86.0	343	1	P2YC_RAT
5	772	43.4	338	1	P2YX_HUMAN
6	741.5	41.7	338	1	P2YX_MOUSE
7	694	39.0	305	1	P2YX_RAT
8	488	27.4	319	1	H963_HUMAN
9	411.5	23.1	375	1	GP34_MOUSE
10	409.5	23.0	381	1	GP34_HUMAN
11	394	22.2	342	1	PAFR_HUMAN
12	392.5	22.1	342	1	PAFR_CAVPO
13	379.5	21.3	361	1	EBI2_HUMAN
14	367	20.6	345	1	CLT2_PIG
15	366	20.6	341	1	PAFR_MOUSE
16	362	20.4	341	1	PAFR_RAT
17	357.5	20.1	308	1	P2Y5_CHICK
18	347.5	19.5	346	1	CLT2_HUMAN
19	347.5	19.5	537	1	P2Y8_XENLA
20	344	19.3	309	1	CLT2_MOUSE
21	339.5	19.1	309	1	CLT2_RAT
22	339	19.1	359	1	AG2R_BOVIN
23	338	19.0	344	1	P2Y5_HUMAN
24	334	18.8	359	1	AG2R_SHEEP
25	334	18.8	367	1	GP17_HUMAN
26	329	18.5	359	1	AG2S_HUMAN
27	328	18.4	340	1	CLT1_PIG
28	327	18.4	359	1	AG2R_PIG
29	326	18.3	359	1	AG2R_CANFA
30	325.5	18.3	399	1	PAR2_MOUSE
31	325	18.3	359	1	AG2R_RABIT
32	321	18.1	359	1	AG2R_MOUSE
33	320	18.0	359	1	AG2R_CAVPO

34	320	18.0	370	1	P2Y9_HUMAN	Q99677 homo sapien
35	319.5	18.0	365	1	GP68_HUMAN	Q15743 homo sapien
36	319	17.9	359	1	AG2R_RAT	P25093 rattus norv
37	319	17.9	359	1	AG2S_RAT	P29089 rattus norv
38	318	17.9	359	1	AG2R_MOUSE	P29754 mus musculu
39	318	17.9	361	1	P2Y4_MOUSE	Q9157 mus musculu
40	316.5	17.8	398	1	OPRM_RAT	P33535 rattus norv
41	316	17.8	359	1	AG2S_MOUSE	P28735 mus musculu
42	316	17.8	377	1	APJ_RAT	Q91hg3 rattus norv
43	316	17.8	397	1	PAR2_RAT	Q63645 rattus norv
44	313.5	17.6	380	1	APJ_HUMAN	P35414 homo sapien
45	313.5	17.6	401	1	OPRM_PIG	Q95247 sus scrofa

ALIGNMENTS

RESULT 1
ID P2YC_HUMAN STANDARD. PRT: 342 AA.
AC Q9H244;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y(ADP))
DE (ADP-glucose receptor) (ADPG-R) (P2Y(AC)) (P2Y(cyc)) (P2Y(AC))
DE (SP1999).
GN P2RY12 OR HORR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21037966; PubMed=11196645;
RA Holoopeter G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA Conley P.B.;
RT "Identification of the platelet ADP receptor targeted by
RT anthrrombotic drugs.";
RT Nature 409:202-207(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RX Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,
RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,
RA Monsie F.J. Jr.;
RT "ADP is the cognate ligand for the orphan G protein-coupled receptor
RT SP1999.";
RT J. Biol. Chem. 276:8608-8615(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=21394281; PubMed=11502873;
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.-I.,
RA Ohishi T., Soga T., Matsushime H., Furuchi K.;
RT "Molecular cloning of the platelet P2Y(AC) ADP receptor:
RT pharmacological comparison with another ADP receptor, the P2Y1
RT receptor.";
RT Mol. Pharmacol. 60:432-439(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Reinisch R.K., Nothacker H.-P., Wang Z., Zeng J., Ehler F.J.,
RA Clevell O.;
RT "ADP-glucose activates a G-protein coupled receptor and inhibits
RT smooth muscle contractions.";
RT Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takeda H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";

```

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RP [6]
RN SEQUENCE FROM N.A.
RC TISSUE-Prostate;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system. Not
CC activated by UDP and GTP. Involved in platelets aggregation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in the platelets, lower
CC levels in the brain. Lowest expressed in the lung, appendix,
CC pituitary and adrenal gland. Expressed in the spinal cord and in
CC the fetal brain.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF313449; AAC48944.1; -
DR EMBL; AF321815; AAK00948.1; -
DR EMBL; AB052684; BAB60824.1; -
DR EMBL; AF310685; AAL32292.1; -
DR EMBL; AB083596; BAB89309.1; -
DR EMBL; BC017898; AAH17898.1; -
DR MIM; 600515; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHOOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1.1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1.2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 25
FT TRANSMEM 26 46
FT DOMAIN 47 58
FT TRANSMEM 59 79
FT DOMAIN 80 99
FT TRANSMEM 100 120
FT DOMAIN 121 142
FT TRANSMEM 143 163
FT DOMAIN 164 191
FT TRANSMEM 192 212
FT DOMAIN 213 233
FT TRANSMEM 234 254
FT DOMAIN 255 281
FT TRANSMEM 282 302
FT DOMAIN 303 342
FT DISULFID 97 175
FT CARBOHYD 6 6
FT CARBOHYD 13 13
SQ SEQUENCE 342 AA; 39438 MM; 8553D2746C89176D CRC64;

```

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Query Match 100.0%; Score 1778; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 1; 5e-112;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 181 EFGLVMEIYNYICQVIFWINEFLIVICVYLITKELYRSYVRIGKVPKRVNVEFI 240
DB 181 EFGLVMEIYNYICQVIFWINEFLIVICVYLITKELYRSYVRIGKVPKRVNVEFI 240
QY 241 IIAVFICFVPHFARIPYLTISQTRDVPDCYAEUTLFYVSESTLWLSNACLDPIYFF 300
DB 241 IIAVFICFVPHFARIPYLTISQTRDVPDCYAEUTLFYVSESTLWLSNACLDPIYFF 300
QY 301 LCKSFNSLSMLCKPNSATSLSDNKRKEQDGDPEDEEPM 342
DB 301 LCKSFNSLSMLCKPNSATSLSDNKRKEQDGDPEDEEPM 342

RESULT 2
P2YC_MACFA STANDARD; PRT; 342 AA.
ID P2YC_MACFA
AC 095KC3; 09BGF8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2RY12.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Frontal cortex, and Medulla oblongata;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB056385; BAB33041.1; -
DR EMBL; AB062981; BAB60747.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHOOPSN.
DR PRINTS; PR01569; P2Y12_PRNCPTR.
DR PRINTS; PR01655; UDPGLUCOSER.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1.1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1.2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 25
FT TRANSMEM 26 46
FT DOMAIN 47 58
FT TRANSMEM 59 79
FT DOMAIN 80 99
FT TRANSMEM 100 120
FT DOMAIN 121 142
FT TRANSMEM 143 163
FT DOMAIN 164 191
FT TRANSMEM 192 212
FT DOMAIN 213 233
FT TRANSMEM 234 254
FT DOMAIN 255 281
FT TRANSMEM 282 302

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FT DOMAIN 303 342 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 173 BY SIMILARITY.
FT CARBOHYD 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 49 49 I -> T (IN REF. 1: BAB33041).
FT CONFLICT 89 89 A -> T (IN REF. 1: BAB33041).
SQ SEQUENCE 342 AA; 39479 MM; E93FC26BBF5EC4C CAC64;

Query Match 98.3%; Score 1748; DB 1; Length 342;
Best Local Similarity 98.0%; Pred. No. 1.5e-110;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQAVDNLSAGNLSLCRDYKRTQVLPFLTYVLFVGLITNGLAMRIFQIRSKSNFI 60
DB 1 MQAIDNLSAGNLSLCRDYKRTQVLPFLTYVLFVGLITNGLAMRIFQIRSKSNFI 60
QY 61 IFLNKTVISDLMLTFPFKILSDAKLGAPLRFVCOVTSVIFFTYISIFGLITI 120
DB 61 IFLNKTVISDLMLTFPFKILSDAKLGAPLRFVCOVTSVIFFTYISIFGLITI 120
QY 121 DRYQTRPFTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCSFLKS 180
DB 121 DRYQTRPFTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCSFLKS 180
QY 181 EFGLVMEIIVYICQVIFWIMFLIYVYTLITKELISYVTRGCVGPKRVKVFYI 240
DB 181 EFGLVMEIIVYICQVIFWIMFLIYVYTLITKELISYVTRGCVGPKRVKVFYI 240
QY 241 IIAVEFICFVFHFRARIPYTLISQTRDVPDCAENLEFVYKSTLMLSLNCLDPIYEF 300
DB 241 IIAVEFICFVFHFRARIPYTLISQTRDVPDCAENLEFVYKSTLMLSLNCLDPIYEF 300
QY 301 LCKSFRLSLMLCKPNSATSLSDNRKEDGGDPNEETPM 342
DB 301 LCKSFRLSLMLCKPNSATSLSDNRKEDGGDPNEETPM 342

RESULT 3
P2YC.MOUSE STANDARD; PRT; 347 AA.
ID P2YC.MOUSE
AC 09CPV9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2RY12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai T., Pesole G., Quackenbush J.,
RA Schirni L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Momberts P.,
RA Notdone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyoko-oka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
```

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RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AK013804; BAB29000.1; -
CC EMBL; AK014807; BAB29561.1; -
CC EMBL; BC025428; AAH25428.1; -
CC EMBL; BC027381; AAH27381.1; -
CC MGD; MGI:1918089; p2ry12.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PRO0237; GPCRHOPOPSN.
CC PRINTS; PRO1569; P2Y12PRNCPTR.
CC PRINTS; PRO1655; UDPGLUCOSER.
CC PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.
CC K-W PROSITE; PS0262; G-protein coupled receptor; Transmembrane; Glycoprotein.
CC TRANSMEM 1 31
CC TRANSMEM 32 52
CC TRANSMEM 53 64
CC TRANSMEM 65 85
CC TRANSMEM 86 105
CC TRANSMEM 106 126
CC TRANSMEM 127 148
CC TRANSMEM 149 169
CC TRANSMEM 170 197
CC TRANSMEM 198 218
CC TRANSMEM 219 239
CC TRANSMEM 240 260
CC TRANSMEM 261 287
CC TRANSMEM 288 308
CC TRANSMEM 309 347
CC DISULFID 103 181
CC CARBOHYD 7 7
CC CONFLICT 3 3
CC CONFLICT 12 12
CC SEQUENCE 347 AA; 39473 MM; F107488E57E025F1 CAC64;

Query Match 87.5%; Score 1555.5; DB 1; Length 347;
Best Local Similarity 88.7%; Pred. No. 1.2e-97;
Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

QY 6 NLSAPGNTSLCTRYKRTQVLPFLTYVLFVGLITNGLAMRIFQIRSKSNFIIFKN 65
DB 12 NLTSPGNTSLCTRYKRTQVLPFLTYVLFVGLITNGLAMRIFQIRSKSNFIIFKN 71
QY 66 TVISDLMLTFPFKILSDAKLGAPLRFVCOVTSVIFFTYISIFGLITTDYQK 125
DB 72 TVISDLMLTFPFKILSDAKLGAPLRFVCOVTSVIFFTYISIFGLITTDYQK 131
QY 126 TTRPRTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCSFLKSEFGY 185
DB 132 TTRPRTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCSFLKSEFGY 191
QY 186 WHEIYNYICQVIFWIMFLIYVYTLITKELISYVTRGCVGPKRVKVFYI 245
DB 192 WHEIYNYICQVIFWIMFLIYVYTLITKELISYVTRGCVGPKRVKVFYI 251
```

Oy	246	FICFEPFHARIPYLSOTRDVDCDTANTETITLYVESTIMTSLNACDPEFYFLCKSF	305
Oy	246	FICFEPFHARIPYLSOTRDVDCDTANTETITLYVESTIMTSLNACDPEFYFLCKSF	305
Db	252	FICFEPFHARIPYLSOTRAVDFCSAENTLFYVESTIMTSLNACDPEFYFLCKSF	311
Oy	306	RNSLISMLKCPNSATSLSDNRRKKRBDGDDPNETPM	342
Db	312	RNSLTSMLRCSNS-TSTSGTNKKKGEGGEPEETPM	347
Db	312	RNSLTSMLRCSNS-TSTSGTNKKKGEGGEPEETPM	347
RESULT 4			
ID	P2YC_RAT	STANDARD:	PRT: 343 AA.
AC	Q9EPX4:		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor).		
GN	P2RY12.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RA	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley;		
RX	MEDLINE=21037966; PubMed=1196645;		
RA	Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,		
RA	Kamakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,		
RA	Conley P.B.;		
RT	"Identification of the platelet ADP receptor targeted by		
RT	anthrombotic drugs.";		
RL	Nature 409:202-207(2001).		
CC	-1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that		
CC	inhibit the adenylyl cyclase second messenger system (by		
CC	similarity).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/		
CC	or send an email to license@sdb-sib.ch).		
CC	-----		
DR	EMBL; AF313450; AAC648945.1; -		
DR	Interpro: IPR000276; GPCR_Rhodpsn.		
DR	Pfam: PF00001; 7tm.1; 1.		
DR	PRINTS: PR000237; GPCRHHODPSN.		
DR	PRINTS: PR01564; OGR1RECEPTOR.		
DR	PRINTS: PR01569; P2Y12PRNCPT.		
DR	PRINTS: PR01655; UDPGLUCOSER.		
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL1; FALSE_NEG.		
DR	PROSITE: PS0262; G-PROTEIN_RECEP_FL2; 1.		
KM	G-protein coupled receptor; Transmembrane; Glycoprotein.		
FT	DOMAIN	1 31	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	32 52	1 (POTENTIAL).
FT	DOMAIN	53 64	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	65 85	2 (POTENTIAL).
FT	DOMAIN	86 105	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	106 126	3 (POTENTIAL).
FT	DOMAIN	127 148	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	149 169	4 (POTENTIAL).
FT	DOMAIN	170 197	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	198 218	5 (POTENTIAL).
FT	DOMAIN	219 239	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	240 260	6 (POTENTIAL).
FT	DOMAIN	261 287	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	288 308	7 (POTENTIAL).
FT	DOMAIN	309 343	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	103 181	BY SIMILARITY.
FT	CARBOHYD	7 7	N-LINKED (GLCNAC. . .) (POTENTIAL).

Seq	CABOHND	12	12	N-LINKED (GLCNAC..)	(POTENTIAL).
FT	SEQUENCE	343 AA:	39047 MM:	7AE0AFCEB6674136	CRC64:
	Query Match	86.0%;	Score 1528.5;	DB 1;	Length 343;
	Best Local Similarity	86.9%;	Pred. No. 7.5e-96;		
	Matches 293;	Conservative 17;	Mismatches 22;	Indels 5;	Gaps 1;
QY	6	NLTSAAGMTSLCTDRKYTKTQVLFLLVYLPFVGLITNGLMRIRFQIRSKSNFIIFLAKN	65		
DB	12	NTTSTIPGTSYLSCKRYKTKTQVLEPLLYLVLEFAGLITSLAMRIFFQIRSKSNFIIFLAKN	71		
QY	66	TVISDLMILTFEPFKILSDAKLGTPRLTFQCVQSVYFETMYTISIFGLITIDRYOK	125		
DB	72	TVISDLMILTFEPFKILSDAKLGAGHLLTLCVQVSYVFETMYTISIFGLITIDRLK	131		
QY	126	TTRPRTSNPKNLGAKILLSVYIMAFMELLSPNNILTRQPRDKNVKCSFLKSEGLV	185		
DB	132	TTRPRTSSPSNLLGAKILLSVYIMAFMELLSPNNILTRRQPRDKIDIKCSFLKSEGLV	191		
QY	166	WHEIYNYICQVYFMNFIYVCTYLITKELKRSYVFRGKGVPRKKNVAVFIITAVF	245		
DB	192	WHEIYNYICQVYFMNFIYVCTYLITKELKRSYVFRGSAKAPKRVNKKVFIITAVF	251		
QY	246	FICFEPHFARIPYTLSDTRDVEDCTAENTLTFYVSESTLMTLSLNCADPIFYFLCKSF	305		
DB	252	FICFEPHFARIPYTLSDTRAVFDCAENLTLYVSESTLMTLSLNCADPIFYFLCKSF	311		
QY	306	RNSLSIMLKCPNSATSLSDQNRKKRQDGGDPNEETPM	342		
DB	312	RNSLSIMLR-----STSGANKKKQGGDPSEETPM	343		
RESULT 5					
P2YX_HUMAN					
ID	P2YX_HUMAN	STANDARD:	PRT:	338 AA.	
AC	Q15391:				
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUN-2002	(Rel. 36, Last sequence update)			
DE	UDP-glucose receptor (G protein-coupled receptor GPR105).				
GN	GPR105 OR KIAA0001.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=96051387; PubMed=7584026;				
RA	Monmura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,				
RA	Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.,				
RT	"Prediction of the coding sequences of unidentified human genes. I.				
RT	The coding sequences of 40 new genes (K14A0001-K14A0040) deduced by				
RT	analysis of randomly sampled cDNA clones from human immature myeloid				
RT	cell line KG-1."				
RL	DNA Res. 1:27-35(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21426338; PubMed=11524702;				
RA	Joensuu T., Haemelaenen R., Yuan B., Johnson C., Tegelberg S.,				
RA	Gasparini P., Zelante L., Pivola U., Pakarinen L., Lehesjoki A.-E.,				
RA	de la Chapelle A., Sankila E.-M.;				
RT	"Mutations in a novel gene with transmembrane domains underlie Usher				
RT	syndrome type 3."				
RL	Am. J. Hum. Genet. 69:673-684(2001).				
RN	[3]				
RP	FUNCTION.				
RX	MEDLINE=20219108; PubMed=10753868;				
RA	Chambers J.K., Macdonald L.E., Sarau H.M., Ames R.S., Freeman K.,				
RA	Foley J.-J., Zhu Y., McLaughlin M.M., Muddock P., McMillan L.,				
RA	Trilli J., Swift A., Ayar N., Taylor P., Vawter L., Nahed S.,				
RA	Szelecs F., Hervey G., Scott C., Watson J.M., Murphy A.-J., Duzic E.,				
RA	Klein C., Bergsma D.-J., Wilson S., Alavi G.P.;				

```

RT   RT "A G protein-coupled receptor for UDP-glucose." ;
FL   FL J. Biol. Chem. 275:10767-10771(2000).
CC   CC -1- FUNCTION: Receptor for UDP-glucose and other UDP-sugar coupled to
CC   CC G-proteins. Not activated by ATP, ADP, UTP or APP.
CC   CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC   CC -1- TISSUE SPECIFICITY: Highest expression in the placenta, adipose
CC   CC tissue, stomach and intestine, intermediate levels in the brain,
CC   CC spleen, lung and heart, lowest levels in the kidney.
CC   CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   CC -----
CC   CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   CC or send an email to license@isb.slb.ch).
CC   CC -----
CC   CC EMBL: D13626; BAA02791.1; -.
DR   DR EMBL; AF456925; AAL47764.1; -.
DR   DR Genew; HGNC:16442; GPRI05.
DR   DR InterPro; IPR000276; GPCR_hodpsn.
DR   DR Pfam; PF00001; 7tm_1; 1.
DR   DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; FALSE_NEG.
DR   DR PROSITE; PSS0262; G_PROTEIN_REC_P2.1; .
KM   KM G-protein coupled receptor: Transmembrane; Glycoprotein.
FT   FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
FT   FT TRANSMEM 30 50 EXTRACELLULAR (POTENTIAL).
FT   FT DOMAIN 51 55 CYTOPLASMIC (POTENTIAL).
FT   FT TRANSMEM 56 76 CYTOPLASMIC (POTENTIAL).
FT   FT DOMAIN 77 96 EXTRACELLULAR (POTENTIAL).
FT   FT TRANSMEM 97 117 CYTOPLASMIC (POTENTIAL).
FT   FT DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).
FT   FT TRANSMEM 140 160 EXTRACELLULAR (POTENTIAL).
FT   FT DOMAIN 161 188 EXTRACELLULAR (POTENTIAL).
FT   FT TRANSMEM 189 209 CYTOPLASMIC (POTENTIAL).
FT   FT DOMAIN 210 234 CYTOPLASMIC (POTENTIAL).
FT   FT TRANSMEM 235 255 EXTRACELLULAR (POTENTIAL).
FT   FT DOMAIN 256 278 EXTRACELLULAR (POTENTIAL).
FT   FT TRANSMEM 279 299 CYTOPLASMIC (POTENTIAL).
FT   FT DOMAIN 300 338 CYTOPLASMIC (POTENTIAL).
FT   FT DISULFID 94 172 BY SIMILARITY.
FT   FT CARBOHYD 3 3 N-LINKED (GLCNAc. .) (POTENTIAL).
FT   FT CARBOHYD 161 161 N-LINKED (GLCNAc. .) (POTENTIAL).
SQ   SQ SEQUENCE 338 AA; 38971 MW; 8DBE7C782CB4753D CRC64;
Query Match 43.4%; Score 772; DB 1; Length 338;
Best Local Similarity 47.5%; Pred. No. 3.3e-45;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0.
QY    QY 6 NLTSAPGNTSLCTRDYKTYOVLLPYLVLPFGVGLITNGLARIFEQIARKSNFIIFLN 65
Db    Db 3 NSTSPGPDESOSQLLTIOIIIPVLQCMVFAGILNLSVGMIFFPVSSAFIITLYKN 62
QY    QY 66 TVISDLMLITLPPFKITSDAKIGTGPLRVCQTVSYFFPMYISISLGITIDRYOK 125
Db    Db 63 IVIADEPVMSLTFPEPKILDGSGPGMQLNVFCRSVAIVLFYVMYYSIVFEGLISPDYRK 122
QY    QY 126 TTRPKTSPNKNLGAKILTSYVIAFMFLLSIPNNILNRQGRDNVKRCSPFLSKSEGLV 185
Db    Db 123 IVKPLMTSFIDSQSILKSILSVYMMMLMLLLANPNILITNQSVREYTIQCIELKSELGKR 182
QY    QY 186 WHEIYNVLCQVIFWINFELIVCYALLIKELRSVVRTRGVGRKKVKNVVEFIITAVF 245
Db    Db 183 WHKASNYLEFAVIEFWVFLILLIVETAIIRKKIFKSHLKSRNSTSVYKXKSSRIIFSIVEF 242
QY    QY 246 FICEVPEHFARIPTYLSTQRDVFDCTALENTLEYKESTLMTLNSLANCDPIFYFLCKSF 305
Db    Db 243 FCEVPEHVIARIPTYSQTEAHYSQSKSEILRYKMEETILLSAANYCDDPIIFYFLCQGF 302
QY    QY 306 RNSLSMLKCPNSA 319
Db    Db 303 REILCKKLHIPLKA 316

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RESULT 6
P2YX_MOUSE
ID P2YX_MOUSE STANDARD: PRT: 338 AA.
AC Q9ESG6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE UDP-glucose receptor (G protein-coupled receptor GPR105).
GN GPR105.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee B.C., Scadden D.T.;
RT "7 transmembrane G protein coupled receptor from hematopoietic
RT progenitors.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for UDP-glucose coupled to G-proteins (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sdb.ch).
CC -----
CC CC EMBL; AF177211; AACG9275.1; -
CC CC MGP; MGI:2155705; Gpr105.
CC CC InterPro: IPR000276; GPCR_Rhodopsn.
CC CC Pfam; PF00001; 7tm_1; 1
CC CC PRINTS; PR00237; GPCR_RHODOPSN.
CC CC PRINTS; PR01569; P2Y12PRNCRPT.
CC CC PRINTS; PR01655; UDPGLUCOSER.
CC CC PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
CC CC PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
CC CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC CC DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 30 50 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 51 55 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 56 76 2 (POTENTIAL).
CC CC TRANSMEM 77 96 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 97 117 3 (POTENTIAL).
CC CC TRANSMEM 118 139 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 140 160 4 (POTENTIAL).
CC CC TRANSMEM 161 188 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 189 209 5 (POTENTIAL).
CC CC TRANSMEM 210 234 CYTOPLASMIC (POTENTIAL).
CC CC TRANSMEM 235 255 6 (POTENTIAL).
CC CC TRANSMEM 256 278 EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 279 299 7 (POTENTIAL).
CC CC TRANSMEM 300 338 CYTOPLASMIC (POTENTIAL).
CC CC DISULFID 94 172 BY SIMILARITY.
CC CC CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC SEQUENCE 338 AA; 38861 MW; 4376B50622A68A4E CRC64;

Query Match 41.7%; Score 741.5; DB 1; Length 338;
Best Local Similarity 44.1%; Pred. No. 3,6e-43;
Matches 146; Conservative 69; Mismatches 109; Indels 7; Gaps 3.

4 VNTLSAGNTSLGCRDYITIQVLEPLLYTVEFGLINGLAMRFPRQIRSKSNITFL 63
DB 1 MNNSTTTDPNCPQSMNLTILQITLIVLKGWVITGLLNGISGWVTFVPPSSKFTIYL 60
64 KNTVSLDLMLITFPFKILSDAKLTGRLRTVCQTVSYIEFTWVISISFGLITIDRY 123

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Db	61	KNIVAAFLMGLTPEPFVKLSDGSGIPQVNVNVCRAVSATFVYVMVYSIVFFGGLISDRY	120
Qy	124	QKTTAPKPTSNPKLLDLAKILISVYIMAFMFLSLPNNILINRQDRDKNVAKCSPLKSEFG	183
Db	121	YKIVKPLLTSLVQSVNRSKLLSLVYMMMLMLLNPNIILINQGVKVEYTKIQCMELKNELG	180
Qy	184	LVMEIYNYICQVIFWTFNFIIVCYTLITKELYSRYSPTRGKGVKVRKNVKNVFPIIA	243
Db	181	RKMRAASNIFYVSLFVFWFLLLIYFATIRTKIFSLKSRKSTSVYKRRSSRNIFSVL	240
Qy	244	VFFICFEPFHEARIPYTLSDRDVFCDTAETLTFFVYESTLMLTSLNACDPIFYFIYELCK	303
Db	241	VFVVCFCFPHYHARIPRYKTSQEGHYSCKRTKETLLYLAKEFTLLSAANVCDDPIFYFLCQ	300
Qy	304	SFR---NSLSM-LKCPNSATSLSDQNRKKE	330
Db	301	PFREYLNKKLLMSLKVON---DEVSVKTRHE	328

ID	P2YX_RAT	STANDARD;	PRT;	305 AA.
AC	O35881;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	UDP-glucose receptor (G protein-coupled receptor GPR105) (YFR 15-20).			
GN	GPR105.			
OS	Rattus norvegicus (Rat).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RA	CHARLTON M.E., WILLIAMS A.S., FOGLIANO M., SWEETNAM P.M., DUMAN R.S.;			
RL	SUBMITTED (OCT-1996) TO THE EMBL/GENBANK/DBJ DATABASES.			
CC	-1- FUNCTION: Receptor for UDP-glucose coupled to G-proteins (By			
CC	similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U76206; BAB71745.1; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PROSITE; PS00237; G-PROTEIN_RECP_FL_1; FALSE_NEG.			
DR	PROSITE; PSS0262; G-PROTEIN_RECP_FL_2; 1.			
KW	G-Protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 29			
FT	TRANSMEM 30 50			
FT	TRANSMEM 51 55			
FT	DOMAIN 56 76			
FT	TRANSMEM 77 96			
FT	DOMAIN 97 117			
FT	TRANSMEM 118 139			
FT	DOMAIN 140 160			
FT	TRANSMEM 161 188			
FT	DOMAIN 189 209			
FT	TRANSMEM 210 234			
FT	DOMAIN 235 255			
FT	TRANSMEM 256 278			
FT	DOMAIN 279 299			
FT	TRANSMEM 300 305			
FT	DOMAIN 306 311			
FT	CARBOHYD 3 3			
FT	CARBOHYD 161 161			

[illegible]

RESULT 8	ID	NAME	STANDARD	PRT	319 AA.
AC	H963_HUMAN	STANDARD			
AC	014626				
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Probable G protein-coupled receptor H963.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
OR	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Peripheral blood monocytes;				
RX	MEDLINE=98036061; PubMed=9370294;				
RA	Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,				
RA	Golden-Fleet M., Kelleher K., Kriz R., LaValle E.R., Metberg D.,				
RA	Spaulding V., Stover J., Williamson M.J., McCoy J.M.;				
RT	"A genetic selection for isolating cDNAs encoding secreted proteins.";				
RL	Gene 198:289-296(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21426338; PubMed=11524702;				
RA	Joensuu T., Haemaelaenen R., Yuan B., Johnson C., Tegelsberg S.,				
RA	Gasparini P., Zelante L., Piroola U., Pakarinen L., Lehesjoki A.-E.,				
RA	"Mutations in a novel gene with transmembrane domains underlie usher				
RT	syndrome type 3.";				
RL	Am. J. Hum. Genet. 69:673-684(2001).				
CC	-1- FUNCTION: ORPHAN RECEPTOR.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
DR	EMBL; AF002986; AAC51846.1; -				
DR	EMBL; AF411849; AAL47763.1; -				
DR	InterPro; IPR000276; GPCR_Rhodopsn.				


```

ID      GP34_HUMAN          STANDARD:          PRT:          381 AA.
AC      G09PC5: 095853;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Probable G protein-coupled receptor GPR34.
GN      GPR34.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC      NCBI_taxid:9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Fetal brain;
RX      MEDLINE=99326137; PubMed=10395919;
RA      Schoneberg T., Schulz A., Grosse R., Schade R., Henklein P.,
RT      Schultz G., Gudermann T.;
RL      "A novel subgroup of class I G-protein-coupled receptors.";
RN      Blochm. Biophys. Acta 1446:57-70(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99156852; PubMed=10036181;
RA      Marchese A., Savzadargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
RT      Im D.-S., Lynch K.R., George S.R., O'Dowd B.F.;
RL      "Discovery of three novel orphan G-protein-coupled receptors.";
RN      Genomics 56:12-21(1999).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20434921; PubMed=10982042;
RA      Jacobl F.K., Broghammer M., Pesch K., Zrenner E., Berger W.,
RT      Meindl A., Pusch C.M.;
RL      "Physical mapping and exclusion of GPR34 as the causative gene for
RN      congenital stationary night blindness type 1.";
RN      Hum. Genet. 107:89-91(2000).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RA      Isoqal T., Oca I., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RT      Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA      Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RT      Arima M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA      Kakumatsu A., Nakamura Y., Nagahari K., Masuo Y., Oshima A.;
RT      "NDO human cDNA sequencing project.";
RL      Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RA      Strausberg R.;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN      [6]
RP      FUNCTION: ORPHAN RECEPTOR.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -1- TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF039686; AAD50531.1; -
DR      EMBL; AF118670; AAD17248.1; -
DR      EMBL; AK027780; BA855362.1; -
DR      EMBL; BC020678; AAR20678.1; -
DR      Genew; HGNC:4490; GPR34.
DR      MIM; 300241; -
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm.1; 1.
DR      PRINTS; PR00237; G_PROTEIN_RECPE_FL_1; 1.
DR      PROSITE; PS00237; G_PROTEIN_RECPE_FL_1; 1.

```

DR PROSITE: PS50262; G-PROTEIN RECEPTOR; Transmembrane; Glycoprotein.
 KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 61 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 62 82 1 (POTENTIAL).
 FT DOMAIN 83 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 89 109 2 (POTENTIAL).
 FT DOMAIN 110 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 3 (POTENTIAL).
 FT DOMAIN 150 171 3 (POTENTIAL).
 FT TRANSMEM 172 192 4 (POTENTIAL).
 FT DOMAIN 193 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 237 5 (POTENTIAL).
 FT DOMAIN 238 269 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 270 290 6 (POTENTIAL).
 FT DOMAIN 291 310 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 311 331 7 (POTENTIAL).
 FT DOMAIN 332 381 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 127 204 BY SIMILARITY.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 181 181 L -> V (IN REF. 1).
 SQ SEQUENCE 381 AA; 43860 MM; 491FC0165624379 CMC64.

 Query Match 23.0%; Score 409.5; DB 1; Length 381;
 Best Local Similarity 32.3%; Pred. No. 6.8e-21;
 Matches 102; Conservative 53; Mismatches 152; Indels 9; Gaps 7;

 QY 2 GAVDNLGAPGNTSICPTDVKYITQVLFLLATYVLFVGLINGLAMRIFFQIRKSNFI- 60
 DB 32 QPPOFESATP-NATTCPPDEKLLSTVLTSSVITVGLVGNIALYVFLGTHRRNSIQ 90
 QY 61 IFLKNTVSDLMILMIFPEFKILSDAKLGTPLFPEFCOVTVSIEFTWYISISFGLITI 120
 DB 91 IYLLNVALADLLILFCLPEFRIMYHINOKMKWGLVCLKAVGGLFPMNMYISIIILGFTSL 150
 QY 121 DRYOKTTRPEKTSNPKNLGAKILSVIWAEMFLLSLPNMILTNQPDKNVKKCSFKS 180
 DB 151 DRYIKINSIQORAKITTKOSIYVCCIWA-MLALGGLFTMILLTKGGHNSMCFHYRD 209
 QY 181 EFGLVWHIVWYIOGVIMINFLIYVCTYLTREKLYR-SIVYRRP-GVGKVPKKVNVK 237
 DB 210 KHNAGGEAIFENFIVMWLLFLLIISYIKIGKNLIRSKRSKFPNSGKATYATARN-- 267
 QY 238 VEIILAVFICFVPPHFAPIRYTTSQTDVEDCAENTLFFYKESLMTLSINACIDPEI 297
 DB 268 SPIVLIITFCFVPRHARFIYISQI-NVSSCYKEIYHKTNEIMLVLSFNSGCLDPVM 326
 QY 298 YFFLCKSFRRNSLSML 313
 DB 327 YFLMSSNIRKIMCOLL 342

 RESULT 11
 PAIR_HUMAN STANDARD; PRT; 342 AA.
 AC P25105;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Platelet activation factor receptor (PAF-R).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=92028922; PubMed=1656963;
 RX Ye R.D., Prossnitz E.R., Zou A., Cochran C.G.;
 TY "Characterization of a human CDNA that encodes a functional receptor

RT for platelet activating factor.";
 RL Biochem. Biophys. Res. Commun. 180:105-111(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=92041873; PubMed=1657923;
 RA Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M.,
 Bito H., Seyama Y., Matsumoto T., Noma M., Shimizu T.;
 RT "Molecular cloning and expression of platelet-activating factor
 RT receptor from human leukocytes.";
 RL J. Biol. Chem. 266:20400-20405(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92250505; PubMed=1374385;
 RA Kunz D., Gerard N.P., Gerard C.;
 RT "The human leukocyte platelet-activating factor receptor. cDNA
 RT cloning, cell surface expression, and construction of a novel
 RT epitope-bearing analog.";
 RL J. Biol. Chem. 267:9101-9106(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92347886; PubMed=122356;
 RA Seyfried C.E., Schwickart V.L., Godiska R., Gray P.W.;
 RT "The human platelet-activating factor receptor gene (PTAFR) contains
 RT no introns and maps to chromosome 1.";
 RL Genomics 13:832-834(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=93112021; PubMed=1281995;
 RA Sugimoto T., Tsuchimochi H., McGregor C.G., Mutoh H., Shimizu T.,
 Kurachi Y.;
 RT "Molecular cloning and characterization of the platelet-activating
 RT factor receptor gene expressed in the human heart.";
 RL Biochem. Biophys. Res. Commun. 189:617-624(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Behal R.H., Debussche M.S., Olson M.S.;
 RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93192035; PubMed=8383507;
 RA Chase P.B., Halonen M., Regan J.W.;
 RT "Cloning of a human platelet-activating factor receptor gene:
 RT evidence for an intron in the 5'-untranslated region.";
 RL Am. J. Respir. Cell Mol. Biol. 8:240-244(1993).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR. A CHEMOTACTIC
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: M80436; AAA60001.1; -
 DR EMBL: M76674; AAA60002.1; -
 DR EMBL: D10202; BAA01050.1; -
 DR EMBL: M88177; AAA60214.1; -
 DR EMBL: S52624; AAB24695.2; -
 DR EMBL: L07334; AAA60108.1; -
 DR EMBL: S56396; AAB25755.1; -
 DR PIR: JH0479; JH0479. -
 DR PIR: AA0191; AA0191. -
 DR PIR: AA1079; AA1079. -
 DR Genew, HGNC:9582; PTAFR.

DR MW: 173393; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECIP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;
 KM Polymorphism.
 FT DOMAIN 1 16
 FT TRANSMEM 17 38
 FT DOMAIN 39 54
 FT TRANSMEM 55 74
 FT DOMAIN 75 91
 FT TRANSMEM 92 113
 FT DOMAIN 114 133
 FT TRANSMEM 134 155
 FT DOMAIN 156 184
 FT TRANSMEM 185 205
 FT DOMAIN 206 233
 FT TRANSMEM 234 254
 FT DOMAIN 255 276
 FT TRANSMEM 277 296
 FT DOMAIN 297 342
 FT DISLIPD 90 173
 FT CARBOHD 169 169
 FT VARIANT 224 224
 FT VARIANT 338 338
 FT CONFLICT 28 28
 FT CONFLICT 66 66
 FT CONFLICT 95 95
 FT CONFLICT 227 228
 FT CONFLICT 227 228
 FT CONFLICT 247 247
 FT CONFLICT 316 316
 SQ SEQUENCE 342 AA; 39203 MW; 890073C9BBA79228 CRC64;
 Query Match 22.2%; Score 394; DB 1; Length 342;
 Best Local Similarity 32.6%; Pred. No. 6.7e-20;
 Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;
 QY 11 PONTSLCTRDYKITYTOVLPPLTYVLFVGLTNGLAMRFFQIR--SKSNFI-IFLKNTV 67
 DB 3 PDDSHMDESEFRYT--LPPIVYSIIFVLGVANGVLMFAFLYCKKFNFKIMVMTL 60
 QY 68 ISDLMLITFEPKRIISDAKLGCPRTFCVYTSVIEFTWYISIFGLTIDRYOKRT 127
 DB 61 MADMFLFLITPLMIVYVYONQNMWILPKFLCNVAGCLFINTYCSVAFGLVITYNRFQAVT 120
 QY 128 RPEKTSNPKNLGAKILSVIVM----AFMFLSLPNMILTRQPRDK---NVKKCSFLK 179
 DB 121 RIKTKAQNATRKRGISLSIVIVAIVGASVYLIDS--TITVPSDASGSGVATFC-FEH 176
 QY 180 SEFGLVMEIYVYICOVFWINFLVIYCYTLITELRSYVTRNGVGRPKKYNVAVF 239
 DB 177 YEKGSVPVLIHIFLIVFSEFFLVLILFCNLVITRLMQPQOORNAEVRRLAM-VC 235
 QY 240 IIAVFEICQVFEHARIPYTLSDRDVFDCAENTLFFVKESTLMTLSINCLDPEYF 299
 DB 236 TYLAVFIIICFVHHVAVQVLPWTLAEL-GRQDSKFHQAINDAHOVTLCLSTNCVLDPVYC 294
 QY 300 FLCKSFNR-----SLISMLKCPNSAT 320
 DB 295 FLTKKFRKHLTEKPFYSMRSSRKCSNAT 322
 RESULT 12
 PAFR_CAVPO STANDARD: PRT; 342 AA.
 AC P21556;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

DR	EMBL: AB052662; BAB60817.1; -	
DR	InterPro: IPR000276; GPCR_Rhodopsin.	
DR	Pfam: PF00001; 7tm_1; 1.	
DR	PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; FALSE_NEG.	
DR	PROSITE: PS50262; G_PROTEIN_RECIP_F2_1.	
KM	G-protein coupled receptor; Transmembrane; Glycoprotein.	
FT	DOMAIN 1 43	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 44 64	1 (POTENTIAL).
FT	DOMAIN 65 73	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 74 94	2 (POTENTIAL).
FT	DOMAIN 95 124	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 125 145	3 (POTENTIAL).
FT	DOMAIN 146 154	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 155 175	4 (POTENTIAL).
FT	DOMAIN 176 205	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 206 226	5 (POTENTIAL).
FT	DOMAIN 227 246	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 247 267	6 (POTENTIAL).
FT	DOMAIN 268 287	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 288 308	7 (POTENTIAL).
FT	DOMAIN 309 345	CYTOPLASMIC (POTENTIAL).
FT	DISULFID 112 188	BY SIMILARITY.
FT	CARBOHYD 20 20	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 29 29	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 177 177	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 184 184	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE 345 AA; 39410 MW; 5D1B1FB89B95905 CRC64;	
Query Match	20.6%; Score 367; DR 1; Length 345;	
Best Local Similarity	29.0%; Pred. No. 4,4e-18;	
Matches 93; Conservative 72; Mismatches 134; Indels 22; Gaps 9;		
QY	1 MQADVNLTSAGNNTSLCRDYKITQVLEPLLYTVLEFGVLTNGLAMRIFQIRSKSNFI 60	
Db	17 MERSTGLNHNHNSNCSCTENK--REFPIYLVLFVFGALNGSIVFLPKPKYSV 74	
QY	61 -IEKNTVLSDLMLLFPFKI-----LSDAKLGTGRLTFVCOVSVIYFTMYISIF 114	
Db	75 NVFMNLNLISDLLETLTLPFRVDYLLRSGNKNIFGDP-----CRMSYSMTVMYSIYF 129	
QY	115 LGLTIDRYQKTTTPRKFSNPKNLGAKILSVIYMAFELSLPMLITNQPRKKNK 174	
Db	130 LTVLSVAFELTFVPRFLHTTSIKNAAILGVYI--LFMASSVLLKNSSEQDNTL 187	
QY	175 CSFLKSEKGLVWHEIVNYICQV--FWINFLVIVCYTLITKELVRSYVRGCGKPRKK 233	
Db	188 CLELNNS-KVTKLKTMTNVALVCGFVLPFGTSLICYLLITALLKVEYDESGL-RLSIRK 245	
QY	234 VNVKFTIIIAVEFLCQVDFHARIPYTLSTQRDVFDCTAENTLFFVKESTMLTSLNAQL 293	
Db	246 ALIVYIALLIFLCQFDPYHLRFLHLEKAD----KCKRLHKAIVATLLAANSCF 301	
QY	294 DPTIYFELCKSFNLSLSMLK 314	
Db	302 NPFLYFAGENFKDLKSLAR 322	
RESULT 15		
PAFR_MOUSE	STANDARD; PRT; 341 AA.	
ID	PAFR_MOUSE	
AC	OG2035;	
DT	15-JUL-1998 (Rel. 36, Created)	
DT	15-JUL-1998 (Rel. 36, Last sequence update)	
DT	15-JUL-1998 (Rel. 36, Last annotation update)	
DE	Platelet activating factor receptor (PAF-R).	
GN	Mus musculus (Mouse).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

RC STRAIN-129/SV;
RA MEDLINE-96239129; PubMed-8670084;
RA Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T.,
RA Noma M., Shmizu T.;
RT "A murine platelet-activating factor receptor gene: cloning,
RT chromosomal localization and up-regulation of expression by
RT lipopolysaccharide in peritoneal resident macrophages.";
RL Biochem. J. 314:671-678(1996).
CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: D50872; BAA09468.1; -
DR MGD: MGI:106066; Pfaff.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1.1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 16
FT TRANSMEM 17 38
FT TRANSMEM 39 54
FT TRANSMEM 55 74
FT TRANSMEM 75 91
FT TRANSMEM 92 113
FT TRANSMEM 114 133
FT TRANSMEM 134 155
FT TRANSMEM 156 184
FT TRANSMEM 185 205
FT TRANSMEM 206 233
FT TRANSMEM 234 254
FT TRANSMEM 255 275
FT TRANSMEM 276 295
FT TRANSMEM 296 341
FT CARBOHYD 4 4
FT CARBOHYD 159 169
FT DISULFID 90 173
SQ SEQUENCE 341 AA; 39148 MW; CNA8CDDBD8D26897 CRC64;

Query Match 20.6%; Score 366; DB 1; Length 341;
Best Local Similarity 29.9%; Pred. No. 5e-18;
Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

OY 20 DKKTQVLEFLLYVLEFVGLITNGLANRIFQI--RSKSNFI--IEKKNVISDLMLIT 76
DB 10 DSEFRYTLFPIYVSIFILGVANGYVLMVAFNLPYSKLEIKIFMVLNLMADLLFLIT 69
OY 77 FPFILISAKIGTGPLRTFVQVSVIFFTMYISISFLGLITDRYOKTRPFTSNPK 136
DB 70 LPLMIVYYNNEGDLPLNFCVAGCLEFINTYCSVAFLGVITNRYQAVAVPIKTAQAT 129
OY 137 NLGAKILSVIYAFM-----FLSLPMILITNROPDRKNKCSFLKSEFG---LVNHE 188
DB 130 TRKRGISLSLIWISYIATATSTNLVPKDGSGNITRCPEHEPEYSPILVAVH 189
OY 189 IVNIIQVYIEMINFLI-VIYCYTLITKELYSYVTRGVGVPKRKVVVFIIIAVPEI 247
DB 190 FIARCFELVFLFYCNVLIHTLITQPMRQ--RKAGV---KRALMNVCTVLAVFII 243
OY 248 CFVPHFARIRITYLSQTDVDFDCTAENTLIFYKESTLMLTSLNACLDPFIYFLCKSRN 307

DB 244 CFVPHHVQVLPMTLAEIG--YQNFHOAINDAHQITLCLSTNCVLDVYICFLTKFRK 301
OY 308 -----SLISMLKCPNSATS 321
DB 302 HISEKFTYMRSSRC-SRATS 321

Search completed: December 6, 2002, 10:04:55
Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:12 ; Search time 101 Seconds

(without alignments)
697.704 Million cell updates/sec

Title: US-09-835-922-2

Perfect score: 1778

Sequence: 1 MQAVDNTSAPGNTSLCTRD.....SQDNKKKQDGGDPNETTPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	829	46.6	333	4 Q9BPV8	Q9BPV8 homo sapien
2	823	46.3	333	4 Q8TDU7	Q8TDU7 homo sapien
3	794	44.7	337	11 Q9D812	Q9D812 mus musculu
4	699.5	39.3	358	4 Q96J28	Q96J28 homo sapien
5	694.5	39.1	358	4 Q9B721	Q9B721 homo sapien
6	685.5	38.6	359	11 Q99M77	Q99M77 mus musculu
7	559	31.4	228	6 Q9BE53	Q9BE53 macaca fasc
8	553.5	31.1	269	4 Q9BXC2	Q9BXC2 macaca fasc
9	448	25.2	176	4 Q9B761	Q9B761 homo sapien
10	388.5	21.9	342	6 Q9T715	Q9T715 bos taurus
11	387.5	21.8	342	6 Q9GK76	Q9GK76 capra hircu
12	368.5	20.7	296	6 Q9TYV6	Q9TYV6 canis famill
13	365	20.5	342	6 Q9XSD4	Q9XSD4 sus scrofa
14	356	20.0	374	13 Q57466	Q57466 melalegris g
15	343	19.3	359	13 Q9PYV7	Q9PYV7 anguilla an
16	338	19.0	359	6 Q9N0U1	Q9N0U1 ovula arles

17	336	18.9	309	11 Q8R528	Q8R528 mus musculu
18	322	18.1	359	11 Q9EP3	Q9EP3 cavia porce
19	321	18.1	359	6 Q9GLN9	Q9GLN9 pan troglod
20	318.5	17.9	399	11 Q8R311	Q8R311 mus musculu
21	318	17.9	359	4 Q8TBK4	Q8TBK4 homo sapien
22	314	17.7	400	6 Q95M54	Q95M54 macaca fasc
23	309	17.4	358	13 Q9PUA0	Q9PUA0 acipenser r
24	309	17.4	454	4 Q9H573	Q9H573 homo sapien
25	307	17.3	359	11 Q9EGR9	Q9EGR9 meriones un
26	304.5	17.1	390	11 Q8V171	Q8V171 mus musculu
27	304.5	17.1	391	11 Q8V170	Q8V170 mus musculu
28	304.5	17.1	393	11 Q8V1M0	Q8V1M0 mus musculu
29	304.5	17.1	401	11 Q9R1P9	Q9R1P9 mus musculu
30	304.5	17.1	408	11 Q8V1P9	Q8V1P9 mus musculu
31	304.5	17.1	439	11 Q9R0D1	Q9R0D1 mus musculu
32	304.5	17.1	444	11 Q9J1Y1	Q9J1Y1 mus musculu
33	301.5	17.0	377	13 Q98U14	Q98U14 brachydanio
34	301.5	17.0	390	13 Q8Q6G4	Q8Q6G4 carassius a
35	300	16.9	384	13 Q98U01	Q98U01 brachydanio
36	299.5	16.8	352	6 Q9TV45	Q9TV45 cercopithec
37	298	16.8	358	13 Q9YGC3	Q9YGC3 xenopus lae
38	297.5	16.7	339	6 Q9TUS5	Q9TUS5 papio cynoc
39	297	16.7	352	6 Q9TV47	Q9TV47 cercopithec
40	296.5	16.7	361	11 Q8VHP3	Q8VHP3 cavia porce
41	294	16.5	343	11 Q9QW32	Q9QW32 rattus sp.
42	293.5	16.5	352	6 Q9TV43	Q9TV43 cercopithec
43	293	16.5	362	11 Q9JLZ0	Q9JLZ0 rattus norv
44	292.5	16.5	352	6 Q9TS07	Q9TS07 cercopithec
45	291.5	16.4	339	6 Q9TSN3	Q9TSN3 macaca fasc

ALIGNMENTS

Q9BPV8	1	PRELIMINARY:	PRT:	333 AA.
AC	Q9BPV8			
AC	Q9BPV8			
DT	01-JUN-2001 (TREMBlrel. 17, Created)			
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	Putative G-protein-coupled receptor FKSg77 (G-protein coupled receptor GPR86).			
DE	GPR86) (G protein-coupled receptor) (G protein-coupled receptor			
GN	FKSg77 OR GPR86 OR GPR94.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEART;			
RA	Wang Y., Gong L.;			
RT	"Molecular cloning of FKSg77, a novel gene encoding a putative G-			
RT	protein-coupled receptor.";			
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.			
RM	[2]			
RM	SEQUENCE FROM N.A.			
RA	MEDLINE-21172992; PubMed-11273702;			
RA	Wittenberger T., Schaller H.C., Hellbrand S.;			
RT	"An expressed sequence tag (est) data mining strategy succeeding in			
RT	the discovery of new G-protein coupled receptors.";			
RL	J. Mol. Biol. 307:799-813(2001).			
RM	[3]			
RM	SEQUENCE FROM N.A.			
RA	MEDLINE-21458557; PubMed-11574155;			
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arkhltko O.,			
RA	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;			
RT	"Discovery and mapping of ten novel G protein-coupled receptor			
RT	genes.";			
RL	Gene 275:83-91(2001).			
RM	[4]			
RM	SEQUENCE FROM N.A.			

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RX PubMed=11546776;
RA Commun D., Gonzalez N.S., Dethaux M., Brezillon S., Lannoy V.,
RA Parmentier M., Boeynaems J.M.;
RT "Identification of a Novel Human ADP Receptor Coupled to G1.";
RL J. Biol. Chem. 276:41479-41485(2001).
DR EMBL: AF345565; AAK29068.1; -.
DR EMBL: AF295368; AAK01664.1; -.
DR EMBL: AF411113; AAL26484.1; -.
DR EMBL: AF406692; AAL01038.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 333 AA; 38440 MW; F234AB50016DF34 CRC64;

Query Match 46.6%; Score 829; DB 4; Length 333;
Best Local Similarity 49.18; Pred. No. 7e-66;
Matches 153; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

QY 17 CTDRYKITQVLPPLLYVLFVGLITNGLAMRIFQIRSKSNFTILEKNTVISDLMLIT 76
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 15 CPDRTRIVQLVFPALYVFLTGILNTLALMVFHIPSSTFIITLKNTLVADLIMTLM 74

QY 77 FPFKILSDAKIGTGLRFVCGVSVIFPFMYISISFLGITTDROKTRPREKTSNPK 136
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 75 LPEKILSDSHLAPWQLRAVCRFSSVIFETMYGVIGLGLADRFKILIRPLRNIFLK 134

QY 137 NLGAKILSVYIMAFMFLSLPNMILTNROPDRKNVCKSLKSEFGVMEHYNYICQV 196
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 135 KPVAKIVSIIIFWFLFISLPNTLSKKEATPSSVKCAKLGKLGKHWQNNNICQF 194

QY 197 IFWIFLIVCYTLIKELYSYVRTRGVGKVPKKVNVKVFIIIAVFICFVPEHFR 256
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 195 IFWVFILMLVFYVYIAKKVYDSYRKSCKRNNKKLEGVFVVAVFVCFAPFHRAR 254

QY 257 IPTYLSOTRDVCTAENTLFYVESITMLTSLNACDPIFYFLCKSFNSLSMKCP 316
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 255 VPYHSQTNNTDCLRNQQLFAKETTLFLAATNICMDPLIYIFLCKKFTKLPQMG--G 312

QY 317 NSATSLSDNNRKKED 332
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 313 RKTASSQENHSSQTD 328

RESULT 2
Q8TDU7 PRELIMINARY; PRT; 333 AA.
AC Q8TDU7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative G-protein coupled receptor.
GN GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RT "SEQUENCE FROM N.A.
RA Takeba S., Kadowaki S., Haga T., Takaue H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RL genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB083597; BAB89310.1; -.
KW Receptor.
SQ SEQUENCE 333 AA; 38409 MW; 3F8BE7EAC8F5428F CRC64;

Query Match 46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 2.4e-65;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

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QY 17 CTDRYKITQVLPPLLYVLFVGLITNGLAMRIFQIRSKSNFTILEKNTVISDLMLIT 76
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 15 CPDRTRIVQLVFPALYVFLTGILNTLALMVFHIPSSTFIITLKNTLVADLIMTLM 74

QY 77 FPFKILSDAKIGTGLRFVCGVSVIFPFMYISISFLGITTDROKTRPREKTSNPK 136
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 75 LPEKILSDSHLAPWQLRAVCRFSSVIFETMYGVIGLGLADRFKILIRPLRNIFLK 134

QY 137 NLGAKILSVYIMAFMFLSLPNMILTNROPDRKNVCKSLKSEFGVMEHYNYICQV 196
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 135 KPVAKIVSIIIFWFLFISLPNTLSKKEATPSSVKCAKLGKLGKHWQNNNICQF 194

QY 197 IFWIFLIVCYTLIKELYSYVRTRGVGKVPKKVNVKVFIIIAVFICFVPEHFR 256
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 195 IFWVFILMLVFYVYIAKKVYDSYRKSCKRNNKKLEGVFVVAVFVCFAPFHRAR 254

QY 257 IPTYLSOTRDVCTAENTLFYVESITMLTSLNACDPIFYFLCKSFNSLSMKCP 316
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 255 VPYHSQTNNTDCLRNQQLFAKETTLFLAATNICMDPLIYIFLCKKFTKLPQMG--G 312

QY 317 NSATSLSDNNRKKED 332
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 313 RKTASSQENHSSQTD 328

RESULT 3
Q9DB12 PRELIMINARY; PRT; 337 AA.
AC Q9DB12;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 2010001106Rik protein.
GN GPR86 OR 2010001106RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RT "SEQUENCE FROM N.A.
RA SPRAIN-C57BL/6J; TISSUE=SMALL INTESTINE.
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya K., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Schenwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK008013; BAB25409.1; -.
DR MGD: MGI:1921441; Gpr86.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 337 AA; 38693 MW; 2C1A76FBF893D5EA CRC64;

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Query Match          44.7%; Score 794; DB 11; Length 337;
Best Local Similarity 45.9%; Pred. No. 9.1e-63;
Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps 3;

OY 6 NUTSAPG--NTSLCTRDYKITOVLPFLTYVLEFVGLITNGLAMRIFFQIRKSNFIIFL 63
DB 6 NTTGQGRKRSRCRCDRIKMTOLPFLTYVLEFVGLITNGLAMRIFFQIRKSNFIIFL 65
OY 64 KNTVSDLMILTFPPKILSDAKLCTGTLRFVCQVTSVIEFYEMYSISFGLITIDRY 123
DB 66 KNTLVADLIMLMLFPKILSDSHLAPMQLRGVCTLSVIEFYEMYSISFGLITIDRY 125
OY 124 OKTTPERTSNPKNLGAKILSVIWAFFELSLDPMILITNRPDKNVKCSFKSEFG 183
DB 126 LKIIMPFKTEFKTAFAKTAFTSVISWLSMFISLPMILITNKEAPPSSVKKACASLPLG 184
OY 184 LVMHEIVYICQVITWIMFLIVCYTLITKELYSYVTRGVKPKKVVAFIITA 243
DB 185 LMMHOVSHTCOLIMAFVILMLLFYAVITKVNYSYRKFRKDS--RHKRLKVFIVWA 243
OY 244 VEFICFVPHFARIPYITLSQTRDVDCIAENTLFFVKESTLMTSLNACLDPEIFYFLCK 303
DB 244 VEFVGFARLHPRIPIYITLSQTRNKDKCNLEOLFIAKEATLFLATNTICMDPLIITILCK 303
OY 304 SFRNSLJMLKCPNSATSLSDNRKKEOD 332
DB 304 KFTOKVPCVRWKGKARTAGSSEDHSSQTD 332

RESULT 4
OY 096J28 PRELIMINARY; PRT; 358 AA.
AC 096J28;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CDNA FLJ1878 f1s, clone PLACE100328, weakly similar to probable G
DE protein-coupled receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagaatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Yamamoto J., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Niimura K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027784; BAB5366.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01569; P2Y12PRNCPTR.
DR PROSITE; PS01655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1.1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECPEP_F1.2; 1.
SQ SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;

Query Match          39.3%; Score 699.5; DB 4; Length 358;
Best Local Similarity 42.6%; Pred. No. 2.4e-54;
Matches 140; Conservative 67; Mismatches 113; Indels 9; Gaps 5;

OY 6 NUTSAPG--NTSLCTRDYKITOVLPFLTYVLEFVGLITNGLAMRIFFQIRKSNFIIFL 64
DB 25 NNSDGPGRKNTVL--HNEEDITVLPLVLLIFVASILNLGLAWIFPHIRNKTSFIIFYLK 81
OY 65 NTVISDLMLITLFPFKILSDAKLCTGTLRFVCQVTSVIEFYEMYSISFGLITIDRY 124
DB 65 NTVISDLMLITLFPFKILSDAKLCTGTLRFVCQVTSVIEFYEMYSISFGLITIDRY 124
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DB 82 NTVADLIMLITLFPFKILSDAKLCTGTLRFVCQVTSVIEFYEMYSISFGLITIDRY 141
OY 125 KTRTPEKTSNPKNLGAKILSVIWAFFELSLDPMILITNRPDKNVKCSFKSEFG 184
DB 142 KYVKKFPGSRMNTNIFTYKVLSCVAVIWAFLSLPHIILITNGOPTEDNIDCKSLSPICV 201
OY 185 VMEHIVYICQVITWIMFLIVCYTLITKELYSYVTRGVKPKKVVAFIITA 243
DB 202 KMTAVTVYNSCLFVAIVLILGCIYIAISRYIHK--SNQFISQSSRRKKNQSIYVVA 259
OY 244 VEFICFVPHFARIPYITLSQTRDVDCIAENTLFFVKESTLMTSLNACLDPEIFYFLCK 303
DB 260 VEFTELPHLCRIPEFTESHDLRLDESQKILLYCKEITLFLSACNCLDPIIFYMCR 319
OY 304 SFRNSLJ--SMLKCPNSATSLSDNRKKE 330
DB 320 SFRRLFKKSNIRTSSEIIRSLQSVRSR 348

RESULT 5
OY 09BY21 PRELIMINARY; PRT; 358 AA.
AC 09BY21;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Orphan G protein-coupled receptor 87.
GN GPR87 OR GPR85.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Heilebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new G-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=21438537; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanli W.B., Arkhilo O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF237763; AAK01858.1; -
DR EMBL; AF411114; AAL26485.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PR01655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECPEP_F1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 41435 MW; FDI157293BESD10F CRC64;

Query Match          39.1%; Score 694.5; DB 4; Length 358;
Best Local Similarity 42.2%; Pred. No. 6.8e-54;
Matches 139; Conservative 68; Mismatches 113; Indels 9; Gaps 5;

OY 6 NUTSAPG--NTSLCTRDYKITOVLPFLTYVLEFVGLITNGLAMRIFFQIRKSNFIIFL 64
DB 25 NNSDGPGRKNTVL--HNEEDITVLPLVLLIFVASILNLGLAWIFPHIRNKTSFIIFYLK 81
OY 65 NTVISDLMLITLFPFKILSDAKLCTGTLRFVCQVTSVIEFYEMYSISFGLITIDRY 124
DB 82 NTVADLIMLITLFPFKILSDAKLCTGTLRFVCQVTSVIEFYEMYSISFGLITIDRY 141
OY 135 KTRTPEKTSNPKNLGAKILSVIWAFFELSLDPMILITNRPDKNVKCSFKSEFG 184
```

Db 142 KVKPFGSDSRMTSTFTKRVLSVCVMVIMAVLSLPNILLTGQPFEDNIDHCSKSLSPGLV 201
 185 VMHEIVYICQVIFWIFLVIYCYTLITKELRSYVTRGVGKPRK-KYNAVFEITIA 243
 Db 202 KMHDAVTVYVASCLEFVANVLIGCYIAISRYIHS--SRQFISQSSKRRKHNSIRVVA 259
 244 VFPCVPEFARIPYLTQSOTRDVDCYTAENTLTFYKVESTLMTLSLNACLDPEFYFLCK 303
 Db 260 VFPCVPEFARIPYLTQSOTRDVDCYTAENTLTFYKVESTLMTLSLNACLDPEFYFLCK 319
 304 SFRNSLT--SMKCPNATSLSDNRKKE 330
 Db 320 SFSRRLFKKSNIRTRSEINSLSQVRSRSE 348

RESULT 6

099MT7 PRELIMINARY; PRT; 359 AA.
 AC 099MT7;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE G-protein coupled receptor GPR87.
 GN GPR87.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21172992; PubMed=11273702;
 RA Wittenberger T., Schaller H.C., Hellebrand S.;
 RT "An expressed sequence tag (est) data mining strategy succeeding in
 the discovery of new G-protein coupled receptors.";
 RJ J. Mol. Biol. 307:799-813(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC EMBL: AF295366; AAK01866.1; -;
 DR MGD: MGI:1934133; Gpr87.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PRINTS: PR01655; UDPGLUCOSER.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 359 AA; 41462 MW; 2EB313C273FECDEA CRC64;

Query Match 38.6%; Score 685.5; DB 11; Length 359;
 Best Local Similarity 41.7%; Pred. No. 4.3e-53;
 Matches 136; Conservative 65; Mismatches 120; Indels 5; Gaps 3;

QY 8 TSAAGNTSLCTROKIKOVLEFLLIYTLFVGLTNGLAMIFQISKSNFIIFLKNIV 67
 Db 26 STSGHGKNSLHANKPDTLLPVLIYVAVASILLNGIAVIFPHIRNKTSIFLYLNIV 85
 QY 68 ISDLMLTFEPFKILSDAKLTGDLPTFCOVTVIYFTYVISTISFLGLTIDRYOKTT 127
 Db 86 VADILMLTFEPKIRVNRAGGPMWFEFILLCRYTSVLRYANNYTSIVGLISVDRILKYV 145
 QY 128 RPEFTSNPKNLGAKIISVIAWFMFLISLPMILNRPDRKNVCKSLKSEFGLVMH 187
 Db 146 KPFSDSRMTSTFTKRVLSVCVMVIMAVLSLPNILLTGQPFEDNIDHCSKSLSPGLV 201
 QY 188 EIVNYICQVIFWIFLVIYCYTLITKELRSYVTRGVGKPRK-KYNAVFEITIAVEF 246
 Db 206 MAVTVYVASCLEFVANVLIGCYIAISRYIHS--SRQFISQSSKRRKHNSIRVVAVVF 263
 QY 247 ICEVPEFARIPYLTQSOTRDVDCYTAENTLTFYKVESTLMTLSLNACLDPEFYFLCK 306
 Db 264 TCFLPYLCKRIPFTFSNDRLLDESARKILYCKEMTLFLSACVNCIDPPIYFFMCKSFS 323

QY 307 NSLT--SMKCPNATSLSDNRKKE 330
 Db 324 RLFLKSNIRTRSEINSLSQVRSRSE 349

RESULT 7

09BE53 PRELIMINARY; PRT; 228 AA.
 AC 09BE53;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical protein.
 OC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL CORTEX;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Tero K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056816; BAB39342.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PRINTS: PR01655; UDPGLUCOSER.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN.1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 228 AA; 26356 MW; 47907F5DBEED22C CRC64;

Query Match 31.4%; Score 559; DB 6; Length 228;
 Best Local Similarity 46.7%; Pred. No. 4.9e-42;
 Matches 105; Conservative 40; Mismatches 78; Indels 2; Gaps 1;

QY 108 MYISIFGLITIDRYOKTTPFKTSNPKNLGAKIISVIAWFMFLISLPMILNRP 167
 Db 1 MYGVIVLGLIAFDFELKIITPLNIPFKTYVSFVFWISFFILSLPMILNSKEA 60
 QY 168 RDKNVKCSFLKSEGLWMEIVYICQVIFWIFLVIYCYTLITKELRSYVTRGVG 227
 Db 61 TPSSVKKCASLKGVLGKMHQIVANNISOIFRWVFLVLYVIAKKVDSYRKSMD 120
 QY 228 KVPKKNVAKYFIITIAVFCVPEFARIPYLTQSOTRDVDCYTAENTLTFYKVESTLMT 287
 Db 121 RKNKKLEGKVFVAVAFVCFADFHTRPYVTSQTNKTKDRIQOLFJAKETTLFLA 180
 QY 288 SLNACLDPEFYFLCKSPRNSLISMLKCPNATSLSDNRKKEOD 332
 Db 181 ATNLCMDPLIYFLCKKFTKLPCKMRGKRTIAS--SQENSSQTD 223

RESULT 8

09BXC2 PRELIMINARY; PRT; 269 AA.
 AC 09BXC2;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Putative G-protein-coupled receptor FKS678 (G protein-coupled receptor
 DE 87).
 GN FKS678.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;


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RA Wang Y.-g, Gong L.;
RT "Identification of FKSG78, a novel gene encoding a putative G-protein-
RL coupled receptor.";
RN Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF145566; AAK29069.1; -.
DR EMBL: BC009540; AAH09540.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 269 AA; 31443 MW; 1E7D498EE20717F6 CRC64;

Query Match 31.1%; Score 553.5; DB 4; Length 269;
Best Local Similarity 42.5%; Pred. No. 1.8e-41;
Matches 111; Conservative 50; Mismatches 95; Indels 5; Gaps 3;

QY 73 MLTFPEFRLSDAKLGTPRLTFCQVTSVFYFTMYISISFLGLITIDRYOKTRPEKT 132
DB 1 MLTFPEFRLVHDGFGPMYFKFLCRYSVLEFYANNYSIVGLISIDRYLVKVPFED 60
QY 133 SNPKRLDAKILSYVYNAFMFLSLPNMILTRNOPRDNKVKCSFLGFLVMEHYVY 192
DB 61 SMYSITFTKVLSCVWVYMAVLSLPLNIIITNGOPTEDIHCCSKLSPGLGVKMHYAVY 120
QY 193 ICQVFEWIFNLIVICYLTITKELYSYVRGKGVKPRK-KVNVKVFIIIVFFICEVP 251
DB 121 VNSCLFVAVVILICCYLAISRYIKHS--SRQFISQSSKKRKHNSIRVAVVFFTCFEP 178
QY 252 FHFANIPYTLISQTRVDFDCTAENILFYVKESTLMLTSLNACLDPIFYFLCKSFNSLI- 310
DB 179 YHLCRIPTFFSHLDRLDESQKILYCKEITLFLSACNVCLDPIFYFMCRSFRLPK 238
QY 311 -SMKCPNSATSLSDNKRKE 330
DB 239 KSNIRTRSEISRLSQSVRSRSE 259

RESULT 9
Q9BY61 PRELIMINARY; PRT; 176 AA.
AC Q9BY61;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative G protein-coupled receptor GPCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RT "Molecular cloning of a probable G protein-coupled receptor with three
RL transmembrane domains.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF178982; AAK18752.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 176 AA; 20194 MW; 352FDA2EA70EF9AD CRC64;

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Query Match 25.2%; Score 448; DB 4; Length 176;
Best Local Similarity 46.8%; Pred. No. 2.8e-32;
Matches 81; Conservative 33; Mismatches 57; Indels 2; Gaps 1;

QY 160 MLTRNOPRDKRVKCSFLSEGLVWHEIVNYICQVIFNIFLIYVICYTLITKELYS 219
DB 1 MLTRNKATPSSVKKKCSKPLGLKMHQWNNICQVIFNIFLIYVIVIAKRVDS 60
QY 220 YVTRGVGKVPKRVNVKVFIIIVFFICEVPFHFARIPYTLISQTRVDFDCTAENTLFEV 279
DB 61 YKSKSKRKNKKKXLEKGVFVAVFVCFARFHFARVYTHSQNNKTKDLQNLQFLIA 120
QY 280 KESTLMLTSLNACLDPIFYFLCKSFNSLSMLKCPNSATSLSDNKRKEED 332
DB 121 KETTLFLAATNICMDPLIYIFLCKRTEKRLPCMQ--GRKRTASQENHSSQTD 171

RESULT 10
Q9TTY5 PRELIMINARY; PRT; 342 AA.
AC Q9TTY5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Platelet-activating factor receptor.
GN PAFR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang W.S., Diehl J.R., Roubesh W.E.;
RT "Partial Sequence of Bovine Platelet-Activating Factor Receptor
RL Gene."
RN Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA He B., Tiemann U., Kautz W., Welkard R., Laurent P., Schwerin M.,
RA Schmidt P.;
RT "Molecular characterization of bovine platelet-activating factor
RT receptor transcripts and their detection in different tissues of
RT cattle."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF187321; AAF01439.2; -.
DR EMBL: AJ295321; CAC43290.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1559; DUFFYANTIGEN.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39691 MW; 7C4236205AE937C9 CRC64;

Query Match 21.9%; Score 388.5; DB 6; Length 342;
Best Local Similarity 30.5%; Pred. No. 1e-26;
Matches 101; Conservative 63; Mismatches 136; Indels 31; Gaps 10;

QY 11 PGNLSICTRDYKITYOVLEPLTYLVEFGLITNGLAMRIEFOIRSKSNF---IIFLKNV 67
DB 3 PNNSEFVDSSEFRYT--LPEIFYSIYFVLGVANSYLVAFARLYSPKFKNEIKFIWNV 60
QY 68 ISDLMLITLFFPKILSDAKLGTPRTFCQVTSVFYFTMYISISFLGLITIDRYOKTT 127
DB 61 MADLFLVTLPLMIYIYYNQGMILPKFLCNLAGCFEFTNYTCSVAFLAVITYNRQAVT 120
QY 128 RFKTSNPKNLGAKILSYVYV-----AFMFLSLPMILTNQPR---DKNVKCSF 177
DB 121 RPIKTAQATRRKGLISLIIVSYVAGASVFFVD-----STNRPKTSANITRC-F 174
QY 178 LKSEGLVWHEIVNYICQVIFNIFLIYVICYTLITKELYSYVTRGVGKVPKRVNVK 237

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Db 175 EHYKSGIPVLTITIFVSEFVFLIILFCNLIIIRLLTQOQOIORNNAVKRRALMM- 233
 QY 238 VETIIAVFICFVPEFHARIPYLTISQTRVDCAENTLTFVYKSTLMTSLNCLDFEI 297
 Db 234 VCIVLAVFIICFVPHHVLQVLPMTLAEI-GFODTDFHOAINDAHOVTLCLSTNCVLDPII 292
 QY 298 YFELCKSFNLSLSML-----KCPNSATS 321
 Db 293 YCFLTKKRKHLETKLYSMRESKRC-SRATS 322

RESULT 11

Q9GK76 PRELIMINARY; PRT; 342 AA.
 AC Q9GK76
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Platelet-activating factor receptor.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang W., Diehl J.R., Plumi F.;
 RT "Partial Sequence of Caprine Platelet-Activating Factor Receptor
 RT Gene."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF302764; AAC39982.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01559; DGFYANTIGEN.
 DR PROSITE: PS00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECCEP_F1_2; 1.
 DR KMW Receptor.
 SQ SEQUENCE 342 AA; 39612 MW; 39D9379AED60FD4E CRC64;

Query Match 21.8%; Score 387.5; DB 6; Length 342;
 Best Local Similarity 30.4%; Pred. No. 1.3e-26;
 Matches 102; Conservative 66; Mismatches 127; Indels 41; Gaps 11;

QY 11 PGNTSLCTRDYKITQVLEPLLYLVLFVGLITNGIAMRIFFQIRKSNF---IIFLKNTV 67
 Db 3 PNNSEFRVDSERYT--LEPIFYSIIVFLVGVANGVYLVAFRLVPSKKFNEIKIFMWLT 60
 QY 68 ISDLMLITPFPRKILSDAKLCTGPRFVQVTSVIFFTWYISISFLGLITTDRIQKTT 127
 Db 61 MADLFLFVTLPLMTIVYYNODMILPRFLCNLAGCFEINTYCSVAFLAVITYNRFQAVT 120
 QY 128 RPFKTSNPKNLGAKILSVIVM-----AFMFLSLPNNMLTNRNRP--DKNVKKCSF 177
 Db 121 RPIITTAQATTKRKRGFLSLIIWVSIVGASAFYFLD-----STNSEPKTSSGNTTRC-F 174
 QY 178 LKSEGLWMEIVNYICOVIFWIMNELIVYCYLTITKELYSYVTRGVGKVPKRVNK 237
 Db 175 EHYKSGIPVLTITIFVSEFVFLIILFCNLIIIRLLTQOQOIORNNAVKRRALMM- 233
 QY 238 VETIIAVFICFVPEFHARIPYLTISQTRVDCAENTLTFVYKSTLMTSLNCLDFEI 297
 Db 234 VCIVLAVFIICFVPHHVLQVLPMTLAEI-GFODTDFHOAINDAHOVTLCLSTNCV 292
 QY 293 YFELCKSFNLSLSML-----KCPNSATS 321
 Db 288 LDPITTCFLTKKFKHLETKLYSMRESKRC-SRATS 322

RESULT 12
 Q9TTY6 PRELIMINARY; PRT; 296 AA.
 ID Q9TTY6

AC Q9TTY6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Platelet-activating factor receptor (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang W.S., Diehl J.R., Murphy K.E.;
 RT "Partial Sequence of Canine Platelet-Activating Factor Receptor
 RT Gene."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF186831; AAF01435.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECCEP_F1_2; 1.
 DR KMW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 296 AA; 33902 MW; 5494C0771C45E101 CRC64;

Query Match 20.7%; Score 368.5; DB 6; Length 296;
 Best Local Similarity 29.5%; Pred. No. 5.4e-25;
 Matches 90; Conservative 66; Mismatches 124; Indels 25; Gaps 7;

QY 20 DYKITQVLEPLLYLVLFVGLITNGIAMRIFF--FQIRKSNFIIIFLKNVISDLMLIT 76
 Db 2 DSERYTLEPIYISIIIFLVGVANGVYLVAFACLPYKSKLEIKIFMWLTMADELLFVLT 61
 QY 77 PFPRILSDAKLCTGPRFVQVTSVIFFTWYISISFLGLITTDRIQKTRPKTSMPK 136
 Db 62 LPLMTIYYHGNMILBSEFLCNLAGCFEINTYCSVAFLAVITYNRFQAVT 121
 QY 137 NLGAKILSVIVM-----AFMFLSLPNNMLTNRNRPDKVKKCSFELWHEI 189
 Db 122 TRKRGFLVSLIVVAIYAAASYFILQSTNVPS--KSGSGNITRC-FEHKESVPLI 178
 QY 190 VNYICQVIFWIMNELIVYCYLTITKELYSYVTRGVGKVPKRVNKVFIITAVFICF 249
 Db 179 VHVIFVGLFVFLIFFCNVIIIRLLMQPVLQHNAEVRRALMM-VCTVLAVFIVCF 237
 QY 250 VPFHARIPYLTISQTRVDCAENTLTFY-----VKESTLMTSLNCLDFEIFYELCKS 304
 Db 238 VPHHVLQVLPMTLA-----ELGFQSSSFHOGINDAHOVTLCLSTNCVLDPIITCFLTKK 291
 QY 305 FRNSL 309
 Db 292 FRKHL 296

RESULT 13
 Q9XSD4 PRELIMINARY; PRT; 342 AA.
 ID Q9XSD4

AC Q9XSD4
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Platelet-activating factor receptor.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Diehl J.R., Murphy K.E., Roudgebush W.E.;
 RT "Porcine (Sus scrofa) platelet-activating factor receptor DNA."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF124054; AAD28739.2; -


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Db 146 TCVLIMAFALSLPTALSRDVTINHP--NTVCGTLDK-----HELSHVLALGLM 196
QY 197 ----IFMINPLIVICYTLITKELYS----YVRTGVGVPRKKVNVKVFIIIAVEPIC 248
Db 197 KSVGLFIPFVIIVTCYCLIGRALLERARVQSSRSG-----DEVLQMLAAVVIAPFLC 250
QY 249 FVP---FHEARIPYTLSDTRDVFDCIAENTLFYVKESTLMLTSLNACIDPFIYFFLCKSF 305
Db 251 WVPQIHFHFHV---LALLKVIENCPTLIDIDTALPFTICIAVFNSCMNPILYGFVGRNF 307
QY 306 RNSLISMLKC-PNSA 319
Db 308 RNLRLRLRCGPGSA 322

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Search completed: December 6, 2002, 10:07:59
 Job time : 104 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:11 ; Search time 20 Seconds

(without alignments)
1643.899 Million cell updates/sec

Title: US-09-835-922-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNKKKEDGGDPNERTPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	394	22.2	342	A40191	platelet-activatin
2	392.5	22.1	342	A13638	platelet-activatin
3	379.5	21.3	361	B45680	G protein-coupled
4	366	20.6	341	S63666	platelet-activatin
5	362	20.4	341	S43252	platelet-activatin
6	357.5	20.1	308	I50241	G protein-coupled
7	339	19.1	359	S15403	angiotensin II rec
8	338	19.0	344	T09508	intron 17 purinerg
9	329	18.5	359	I39418	angiotensin II rec
10	326	18.3	359	S44425	angiotensin II rec
11	325.5	18.3	359	I48705	angiotensin II rec
12	325	18.3	359	A48857	proteinkinase activat
13	321	18.1	359	JC1104	angiotensin II rec
14	321	18.1	370	JC5549	heptahelical P2Y5-
15	319	17.9	359	A42656	angiotensin II rec
16	319	17.9	359	JC2134	angiotensin II rec
17	318	17.9	359	JC1194	angiotensin II rec
18	318	17.9	359	JH0621	angiotensin II rec
19	317.5	17.9	365	S68208	G protein-coupled
20	317.5	17.9	398	I56517	mu opioid receptor
21	314.5	17.7	398	I56504	mu opioid receptor
22	314	17.7	359	J01516	angiotensin II rec
23	313.5	17.6	380	I38435	angiotensin II rec
24	310.5	17.5	362	JN0694	angiotensin II rec
25	309	17.4	392	S65693	opioid receptor mu
26	309	17.4	400	I56553	mu opiate receptor
27	306	17.2	397	S66518	proteinkinase-activat
28	304.5	17.1	398	A57510	mu opioid receptor
29	299	16.8	380	JC2434	kappa opioid recep

30	298.5	16.8	365	2	S68679	G protein-coupled
31	298	16.8	380	2	A48227	kappa opioid recep
32	297.5	16.7	359	2	I51372	angiotensin II rec
33	297.5	16.7	360	2	A53611	interleukin-8 rece
34	297	16.7	380	2	A55259	kappa opioid recep
35	296.5	16.7	420	2	I51667	thrombin receptor
36	296	16.6	380	2	S36143	kappa opioid recep
37	295	16.6	380	2	JC2358	kappa opioid recep
38	292.5	16.5	362	2	S33733	G protein-coupled
39	291.5	16.4	373	2	A47556	ATP receptor P2u -
40	290.5	16.3	352	2	A45747	G protein-coupled
41	284.5	16.0	333	2	I38974	protein-coupled
42	282.5	15.9	352	2	G00048	fusin (LESTRA) - c
43	282	15.9	352	2	A43113	chemokine (C-C) re
44	282	15.9	355	2	J01231	interleukin-8 rece
45	281.5	15.8	353	2	S28787	neuropeptide Y/pep

ALIGNMENTS

RESULT 1
A40191
platelet-activating factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 20-Jun-2000
C:Accession: A40191; JH0479; A41079; JC1359; A42831; I51923
R:Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell
A:Reference number: A40191; MUID:92250505; PMID:1374385
A:Accession: A40191
A:Molecule type: mRNA
A:Residues: 1-342 <RNA>
A:Cross-references: GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294
R:Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A:Title: Characterization of a human cDNA that encodes a functional receptor for plat
A:Reference number: JH0479; MUID:92028922; PMID:1656963
A:Accession: JH0479
A:Molecule type: mRNA
A:Residues: 1-342 <YER>
A:Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
A:Experimental source: granulocyte, cell line HL-60 all
R:Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaoka, C.; Mutoh, H.; Minami, M.; Bito, H.;
J. Biol. Chem. 266, 20400-20405, 1991
A:Title: Molecular cloning and expression of platelet-activating factor receptor from
A:Reference number: A41079; MUID:92041873; PMID:1657923
A:Accession: A41079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-342 <NAK>
A:Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BA01050.1; PID:g219976
R:Sugimoto, T.; Tsuchimoto, H.; McGregor, C.G.; Mutch, H.; Shimizu, T.; Kunachi, Y
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A:Title: Molecular cloning and characterization of the platelet-activating factor rec
A:Reference number: JC1359; MUID:93112021; PMID:1281995
A:Accession: JC1359
A:Molecule type: mRNA
A:Residues: 1-315, 'N', 317-342 <SUG>
A:Experimental source: heart
A:Note: the authors translated the codon AAT for residue 316 as Lys
R:Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A:Title: The human platelet-activating factor receptor gene (PTAFR) contains no intro
A:Reference number: A42831; MUID:92347866; PMID:1322356
A:Accession: A42831
A:Molecule type: DNA
A:Residues: 1-226, 'TG', 229-342 <SEY>
A:Cross-references: GB:M8177; NID:g190697; PIDN:AAA60214.1; PID:g190698
R:Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

Db 351 M 351

RESULT 4

S63666 Platelet activating factor receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C/Accession: S63666

R:Shih, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314, 671-676, 1996

A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization

A/Accession: S63666; MUID:96239129; PMID:8670084

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <ISH>

A:Cross-references: EMBL:D50872; NID:91256924; PIDN:BA09468.1; PID:91256925

C:Superfamily: ATP receptor P2u

Query Match 20.6%; Score 366; DB 2; Length 341;

Best Local Similarity 29.9%; Pred. No. 4e-24;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

OY 20 DYKTTQVLEPLLYTVLFVGLITNGLANRIFFQI--RSKSNFI-TLKNVYISDLMLIT 76

Db 10 DSEFRYTLPIYVSIVIFLGVANGVLMVFNALYPSKKLNEIKIFVNLTMADLLFLIT 69

OY 77 FPFKILSAKIGTGPLRTFVCQVSVIFFTMYISISFLGLITIDRYOKTRPFTSNPK 136

Db 70 LPLMIVYYNSGDMILPNEFLCNVAGCLFEINTYCSVAFLGYTVNRYQAVAPITQAOT 129

OY 137 NLGAKILSVIYMAFM-----FLSLPMMILTNROPDRKNVKKCSFLESG--LVWHE 188

Db 130 TRKGISLSLTIWISIVATASYFLATDSTNLVPKDGSNITRCEHEPEPSVPLVAVH 189

OY 189 IVNTICQVIEIMNPLI-VIVCYTLTKELYSRYTRGCVPRKKNVKEFIITAVEFI 247

Db 190 FIACFELVFLIFECNLIIVHTLTQPMRQ--RKAGV---KRRLMVCVLAFLVI 243

OY 248 CFVPHFRIRIYVTSQTRDVEDCTAENTLFYKESTLWLTSLNACLDPIYFLCKSRN 307

Db 244 CFVPHVAVLQWTLAEIG--YQTFHQAINDAHQITCLISTNCVLDPIYICFLTKRERK 301

OY 308 -----SLISMLKCPNSATS 321

Db 302 HLEKFTYMSRSRKC-SRATS 321

RESULT 5

S43252

Platelet-activating factor receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

C/Accession: S43252

R:Bitto, H.; Honde, Z.; Nakamura, M.; Shimizu, T.

Eur. J. Biochem. 221, 211-218, 1994

A:Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-1

A/Accession: S43252; MUID:94222063; PMID:8168510

A:Residues: 1-341 <BIT>

A:Molecule type: mRNA

A:Cross-references: GB:U04740; NID:9470384; PIDN:AA18422.1; PID:9470385

C:Superfamily: ATP receptor P2u

Query Match 20.4%; Score 362; DB 2; Length 341;

Best Local Similarity 28.9%; Pred. No. 8.9e-24;

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

OY 20 DYKTTQVLEPLLYTVLFVGLITNGLANRIFF--FOIRSKSNFIILKNVYISDLMLIT 76

Db 10 DSEFRYTLPIYVSIVIFLGVANGVLMVFNALYPSKKLNEIKIFVNLTMADLLFLIT 69

OY 137 NLGAKILSVIYMAFM-----FLSLPMMILTNROPDRKNVKKC-----S 176

Db 130 TRKGISLSLTIWISIVATASYFLATDSTNLVPKDGSNITRCEHEPEPSVPLVAVH 189

OY 177 FLKSEFGLVWHEIVYICQVIFWIFNLIVCYTLTKELYSRYTRGCVPRKKNV 236

Db 190 FITSCFELVFF-----LIFYCMVITL---HTLTTP-----VRQQRKEVRRALAM 233

OY 237 KVFIIIAVEFICFVPHFRIRIYVTSQTRDVEDCTAENTLFYKESTLWLTSLNACLDPI 296

Db 234 -VCVLAFLAVFICFVPHFRIRIYVTSQTRDVEDCTAENTLFYKESTLWLTSLNACLDPI 290

OY 297 IYFPLCKSFRN-----SLISMLKCPNSATS 321

Db 291 IYCFLTKKFRKHLSEKFTYMSRSRKC-SRATS 321

RESULT 6

150241

G:protein-coupled receptor 6H1 - chicken

N:Alternate names: purinoreceptor 6H1

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000

C/Accession: 150241; J04618

R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

A:Title: Identification of a G protein coupled receptor induced in activated T cells.

A/Reference number: 150241; MUID:93329058; PMID:8393036

A/Accession: 150241

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-308 <KAP>

A:Cross-references: GB:L06109; NID:9304383; PIDN:AA06587.1; PID:9304384

R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

A:Title: Identification of 6H1 as a P2Y purinoreceptor: P2Y5.

A/Reference number: J04618; MUID:96190677; PMID:8619790

A/Accession: J04618

A:Molecule type: mRNA

A:Residues: 1-308 <WEB>

A:Cross-references: GB:L06109; NID:9304383; PIDN:AA06587.1; PID:9304384

A:Experimental source: T-cells

C:Comment: This receptor plays a role in T-cell activation.

C:Genetics:

A:Gene: p2y5

C:Superfamily: ATP receptor P2u

P:15-40/Domain: transmembrane #status predicted <TM1>

P:51-74/Domain: transmembrane #status predicted <TM2>

P:89-109/Domain: transmembrane #status predicted <TM3>

P:133-153/Domain: transmembrane #status predicted <TM4>

P:177-201/Domain: transmembrane #status predicted <TM5>

P:227-248/Domain: transmembrane #status predicted <TM6>

P:265-292/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 357.5; DB 2; Length 308;

Best Local Similarity 29.5%; Pred. No. 1.9e-23;

Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

OY 14 TSLCTRDYKTIQVLEPLLYTVLFVGLITNGLANRIFF--FOIRSKSNFIILKNVYISDL 72

Db 3 SSMCTEDSFYKTYLGVFSNVFVGLTANCAVATIFFTLKVRNRETTTMMNLNLSDL 62

OY 73 MLTPFPKILSDAKIGTGPLRTFVCQVSVIFFTMYISISFLGLITIDRYOKTRPFT 132

Db 63 FVFTELFPRIYVAV--VRNMPFGVDVLCISVTLFTYTMVGSILFLCTISVDRLAIYHPERS 121

OY 133 SNPKNLGAKILSVIYMAFMELSLPMMIL--TNROPDRKNVKK--SFLASEFGLVWHE 188

[illegible][illegible]

Db 319 YIPPKASHSNLSTK 333

RESULT 13

JC1104

angiotensin II receptor type 1 - human
N:Alternate names: angiotensin II receptor 1A

C:Species: Homo sapiens (man)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000

C/Accession: JC1104; J01402; J05074; A44014; S18983

R/Muzy, C.A.; Hwang, O.; Eglhoff, A.M.; Wu, L.H.; Chung, F.Z.

Biochem. Biophys. Res. Commun. 186, 277-284, 1992

A:Title: Cloning, expression, and characterization of a gene encoding the human angioten

A:Reference number: JC1104; MUID:92337608; PMID:1378723

A:Accession: JC1104

A:Molecule type: DNA

A:Residues: 1-359 <MANU>

R/Furuta, H.; Guo, D.F.; Inagami, T.

Biochem. Biophys. Res. Commun. 183, 8-13, 1992

A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type

A:Reference number: J01402; MUID:92181475; PMID:1543512

A:Accession: J01402

A:Molecule type: DNA

A:Residues: 1-359 <FUR>

A:Cross-references: EMBL:Z11162; NID:928709; PID:928710

A:Experimental source: Lymphocyte

R/Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthallagan, P.; Kersten, H.; Elshourbagy, N.; G

Biochem. Biophys. Res. Commun. 183, 989-995, 1992

A:Title: Cloning and characterization of a human angiotensin II type 1 receptor.

A:Reference number: J05074; MUID:92231907; PMID:1567413

A:Accession: J05074

A:Molecule type: mRNA

A:Residues: 1-359 <BER>

A:Cross-references: GB:887290; NID:9178682; PID:AAA35535.1; PID:9178683

A:Experimental source: Liver

R/Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Naka, R.; Yanase, T.; Hagi, M.; Inagami, T.; F

Biochem. Biophys. Res. Commun. 183, 910-916, 1992

A:Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human ty

A:Reference number: J05067; MUID:92198490; PMID:1550596

A:Accession: J05067

A:Molecule type: mRNA

A:Residues: 1-359 <TRA>

A:Experimental source: Liver

R/Curnow, K.M.; Pascoe, L.; White, P.C.

Mol. Endocrinol. 6, 1113-1118, 1992

A:Title: Genetic analysis of the human type-1 angiotensin II receptor.

A:Reference number: A44014; MUID:92375105; PMID:1508224

A:Accession: A44014

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <CUR>

A:Cross-references: GB:M93394; NID:9178680; PID:9178681

C/Genetics: A:Note: sequence extracted from NCBI backbone (NCBIN:111831, NCBI:111833)

A:Gene: GDB:AGT1

A:Cross-references: GDB:132359; OMIM:106165

A:Map position: 3q21-3q25

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane pr

F:30-53/Domain: transmembrane #status predicted <TM1>

F:65-90/Domain: transmembrane #status predicted <TM2>

F:103-124/Domain: transmembrane #status predicted <TM3>

F:145-167/Domain: transmembrane #status predicted <TM4>

F:194-216/Domain: transmembrane #status predicted <TM5>

F:241-264/Domain: transmembrane #status predicted <TM6>

F:281-305/Domain: transmembrane #status predicted <TM7>

F:4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

18.1%; Score 321; DB 2; Length 359;

Best Local Similarity 28.7%; Pred. No. 3.2e-20;

Matches 92; Conservative 56; Mismatches 139; Indels 34; Gaps 9;

OY 26 VLEPLITVLEFVGLITNGL-AMRIFFQIRKSNFFIIFLKNVTISDLMLITPPFKLSD 84

Db 29 VMIPFLYSIIFFVGVIGFNSLSLVVIVFYFMKLTAVSFLLMLALADLCFLITLPLMAVYT 88

OY 85 AKLGTGPLRPFVCOVTSVIEFMTYISISFLGITIDRYOKTTPFRKSNPKNLGAKIL 144

Db 89 AMEYRMPFGNYLCKIASVSEFNILYASVFLITCISIDRIALIVHPKSRRLRLVAKVT 148

OY 145 SVVIAEMFELSLPNNMILT-N-RQPRDKNVKCSF-----LKSEGLVWHEIVNYICQ 195

Db 149 CIIIMLAGLASLPAIIRHNVFIEMNINIVCAHYESQNSLPIGGLT-KNLTGFL-- 205

OY 196 VIFINFLIVVCTLTITKEIYRSYVRTRGVGKVRKKNVKNVFTITAVFICVPPHEA 255

Db 206 ---FPLILITSTYLTWKALKAKVETOK---NKRPRNDIIFKIIIMAVLFEFF-----FS 252

OY 256 RIFYLSQTRDVF-----DCTAENTLFYKESTLMTSLNACLDPIFYFLCKSPRNS 308

Db 253 WIPQITFFLDVLIQLGIIRDCRIADIVDRAMPITITCIAIFNNCLNPLFYGLGKKRRY 312

OY 309 LISMK-CPNSTATSLSDNRK 328

Db 313 FLQLKTYIPPKASHSNLSTK 333

RESULT 14

JC5549

heptahelical p2y5-like receptor - human

C:Species: Homo sapiens (man)

C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999

C/Accession: JC5549

R/Janssens, R.; Boeynaems, J.M.; Godart, M.; Commun, D.

Biochem. Biophys. Res. Commun. 236, 106-112, 1997

A:Title: Cloning of a human heptahelical receptor closely related to the p2y5 recepto

A:Reference number: JC5549; MUID:97366605; PMID:9223435

A:Accession: JC5549

A:Molecule type: DNA

A:Residues: 1-370 <JAN>

A:Cross-references: DDBJ:AF005419; NID:92240034; PID:AB66322.1; PID:92240035

C/Superfamily: ATP receptor P2u

Query Match

18.1%; Score 321; DB 2; Length 370;

Best Local Similarity 27.7%; Pred. No. 3.3e-20;

Matches 87; Conservative 67; Mismatches 134; Indels 26; Gaps 9;

OY 7 LTSAPGNTSLCTRDYKITQVLEPLITVLEFVGLITNGLAMRIP-FQIRKSNFFIIFLKN 65

Db 22 LGNMTANNT-CIYDDSKRYNNGAVSVFIIIGLITNSVSLFVCFKMKRSEIATITN 80

OY 66 TVISDLMILTEPPKIISDAKLGTPRTVYQVTSVIEFTMTISIFGLITIDRYOK 125

Db 81 LAVSDLLFVCTLPKRIEYNN-RHMPFGDTLCKISGTAFLNINIGSMLFLICISVDRFLA 139

OY 126 TTRPKTSNPNKLGAKILSVIAFMFLSLPMMIILNPNRKNKYSFLKSEGL- 184

Db 140 IVYFPRKSTITTRNSAIVCAVWILVLSGISASLEST-----TNVNNMTTCFE-GLS 193

OY 185 --VWHEIVNYICQVIFMINFLIV-----CYTLITKEIYR---SVYRTGCVGKVRPKV 234

Db 194 KRVMKTYLSKTIIEVGVFIIPILAVSCSVLRLRLRPATISQIGTN-----KKVY 247

OY 235 NKVFIITIAVEFICVPPHEARIPYTLISQTRDVEDCTAENTLFYKESTLWLSLNCLD 294

Db 248 LKMTIVMAVAVVGVFVYNSVFLYALVRSQATINCFLEPRAKIMYPITLCLATLNCDFD 307

OY 295 PEIYFFLCKSPRNS 308

Db 308 PEIYFTLESFQKS 321

RESULT 15

A42656

angiotensin II receptor type 1B (AT3) - rat

N:Alternate names: angiotensin II receptor chain B
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence
C:Accession: A42656; S20423
R:Sandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Calt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A:Title: Cloning and expression of a novel angiotensin II receptor subtype.
A:Reference number: A42656; MUID:92250585; PMID:1374402
A:Accession: A42656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SANA>
A:Cross-References: GB:M90065; NID:g202801; PIDN:AAA40704.1; PID:g202802
A:Experimental source: adrenal cortex
A:Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBI:P.100268)
R:Wai, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A:Title: Identification of two subtypes in the rat type I angiotensin II receptor
A:Reference number: S20423; MUID:92183879; PMID:1544458
A:Accession: S20423
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <IYMA>
A:Cross-References: GB:X64052; NID:g57521; PIDN:CAA5410.1; PID:g57522
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

